



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 110491

TO: Dave Nguyen  
Location: CM1/12B15  
Art Unit: 1632  
Monday, December 22, 2003  
Case Serial Number: 09/620607

12E12

From: Paul Schulwitz  
Location: Biotech-Chem Library  
CM1-6B06  
Phone: 305-1954

paul.schulwitz@uspto.gov

### Search Notes

Examiner Nguyen,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(703)305-1954

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:39:45 ; Search time 2124 Seconds  
(without alignments)  
10304.449 Million cell updates/sec

Title: US-09-620-607B-34  
Perfect score: 535  
Sequence: 1 gcagagaacaaatgccaga.....aaaaaatgtccctaactgg 535

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:  
28: em\_un:  
29: em\_vi:  
30: em\_htg\_hum:  
31: em\_htg\_inv:  
32: em\_htg\_other:  
33: em\_htg\_mus:  
34: em\_htg\_pln:  
35: em\_htg\_rod:  
36: em\_htg\_mam:  
37: em\_htg\_vrt:  
38: em\_sy:  
39: em\_htgo\_hum:  
40: em\_htgo\_mus:  
41: em\_htgo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	521.4	97.5	1011	10	BC028879	BC028879 Mus muscu
2	521.4	97.5	180007	2	AC132933	AC132933 Mus muscu
C 3	521.4	97.5	203000	2	AC139212	AC139212 Mus muscu
4	515.8	96.4	1040	10	AF166097	AF166097 Mus muscu
5	514.2	96.1	1040	6	BD095993	BD095993 Immunoass
6	514.2	96.1	1040	6	BD103482	BD103482 Immunoass
7	347.2	64.9	185784	2	AC120860	AC120860 Mus muscu
8	347.2	64.9	208806	2	AC102491	AC102491 Mus muscu
9	296.2	55.4	910	10	AF166100	AF166100 Rattus no
10	296.2	55.4	332220	2	AC128180	AC128180 Rattus no
C 11	146.2	27.3	86186	2	AC133544	AC133544 Homo sapi
12	146.2	27.3	95202	2	AC140524	AC140524 Homo sapi
13	146.2	27.3	117774	2	AC140508	AC140508 Homo sapi
14	146.2	27.3	193633	9	AC009167	AC009167 Homo sapi
15	146.2	27.3	198276	2	AC145040	AC145040 Gorilla g
C 16	144.6	27.0	174634	2	AC140513	AC140513 Homo sapi
17	144.6	27.0	187359	2	AC140518	AC140518 Homo sapi
18	144.6	27.0	196341	2	AC140517	AC140517 Homo sapi
C 19	144.6	27.0	205443	2	AC140505	AC140505 Homo sapi
C 20	144.6	27.0	231174	9	AC139264	AC139264 Homo sapi
C 21	144.6	27.0	241278	9	AC097268	AC097268 Pan trogl
22	131.6	24.6	456	10	AF210429	AF210429 Mus muscu
23	120	22.4	742	6	AR105919	AR105919 Sequence
24	120	22.4	742	6	AR211354	AR211354 Sequence
25	95.2	17.8	1020	6	BD095984	BD095984 Immunoass
26	95.2	17.8	1020	6	BD103473	BD103473 Immunoass
27	95.2	17.8	1020	9	HSU95301	U95301 Human calci
C 28	94	17.6	445	6	AX329696	AX329696 Sequence
C 29	94	17.6	445	6	AX335440	AX335440 Sequence
30	88.4	16.5	159621	9	AC083801	AC083801 Homo sapi
31	87.8	16.4	465	6	BD095985	BD095985 Immunoass
32	87.8	16.4	465	6	BD103474	BD103474 Immunoass
33	86.8	16.2	148116	2	AC078838	AC078838 Homo sapi
34	78.2	14.6	94673	2	AC009018	AC009018 Homo sapi
35	42.6	8.0	156959	2	AC136042	AC136042 Rattus no
36	42.6	8.0	207549	2	AC137021	AC137021 Rattus no
37	42.6	8.0	212000	2	AC106080	AC106080 Rattus no
38	42.6	8.0	308087	2	AC128813	AC128813 Rattus no
C 39	40	7.5	140120	9	AL390237	AL390237 Human DNA
C 40	40	7.5	142126	2	AC026139	AC026139 Homo sapi
C 41	40	7.5	178364	2	AC021702	AC021702 Homo sapi
42	40	7.5	231252	2	AC140137	AC140137 Homo sapi
43	39.4	7.4	220242	10	AL603706	AL603706 Mouse DNA
C 44	38.6	7.2	228000	2	AC115692	AC115692 Mus muscu
C 45	38.2	7.1	290029	1	AE017027	AE017027 Bacillus

ALIGNMENTS

RESULT 1  
BC028879  
LOCUS BC028879 1011 bp mRNA linear ROD 16-APR-2003  
DEFINITION Mus musculus phospholipase A2, group X, mRNA (cdna clone MGC:25894 IMAGE:4218273), complete cds.  
ACCESSION BC028879  
VERSION BC028879.1 GI:22135659  
KEYWORDS MGC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 1011)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1011)

Strausberg,R.

Direct Submission

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 31 Row: b Column: 16

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers

1. .1011

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="MGC:25894 IMAGE:4218273"

/tissue\_type="Colon, normal. 5 month old male mouse."

/clone\_lib="NCI CGAP\_Co24"

/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6"

1. .1011

/gene="Pla2g10"

/note="synonyms: PLA2GX, mGxsPLA2"

/db\_xref="LocusID:26565"

/db\_xref="MGI:1347522"

33. .467

/codon\_start=1

/product="Pla2g10 protein"

/protein\_id="AAH28879.1"

/db\_xref="GI:22135660"

/db\_xref="LocusID:26565"

/translation="MLLLLLLLGPGPFSEATRRSHVYKRLLELAGTLDCVGPES PMAYMNYGCYGLGGHGEPRDAIDWCYHHDCCYSRAQDAGSPKLDRIYPWKCMDHHI

FEATURES

source

gene

CDS

BASE COUNT 263 a 247 c 251 g 250 t

ORIGIN

Query Match 97.5%; Score 521.4; DB 10; Length 1011;

Best Local Similarity 99.6%; Pred. No. 2.1e-156;

Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCAGAGAACAATGCCAAGAACCTTTTGTGCAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60

DB 430 GCAGAGAACAATGCCAAGAACCTTTTGTGCAGGTGTGACGAGGAGCTGGCTTACTGCCTG 489

QY 61 GCAGGGACCGAGTACCACCTGAAATACCTCTTCTTCCCTCCCATTTTATGTGAGAAAGGAC 120

DB 490 GCAGGGACCGAGTACCACCTGAAATACCTCTTCTTCCCTCCCATTTTATGTGAGAAAGGAC 549

QY 121 TCTCCCAAGTGCAATTGACAGGCTCACATGTCCTTTTGCACATGGAAACGCACATT 180

DB 550 TCTCCCAAGTGCAATTGACAGGCTCACATGTCCTTTTGCACATGGAAACGCACATT 609

QY 181 TCAGTGATCACCAACAGCATGCAATTTGTGAGGAGAGTACCCGGAGGCCAAGTGCTAAA 240

DB 610 TCAGTGATCACCAACAGCATGCAATTTGTGAGGAGAGTACCCGGAGGCCAAGTGCTAAA 669

QY 241 GCCACCTGCGTTTGTCTTCTCTCCATTCCAGGAACCTACAACTATGAGCCTGTGGAGTT 300

DB 670 GCCACCTGCGTTTGTCTTCTCTCCATTCCAGGAACCTACAACTATGAGCCTGTGGAGTT 729

QY 301 GCCAGTCTGATGAAGTTCAAAGTCCCTGGCCTGTTTATACAAATAAGCGCTGTGTGG 360

DB 730 GCCAGTCTGATGAAGTTCAAAGTCCCTGGCCTGTTTATACAAAT-AGCGCTGTGTGG 788

QY 361 GCGTGGTATACCTTTTGAAATTCAGCCTTTATGAGAAAGCTGTACTATCTTGTACCTGCTG 420

DB 789 GCGTGGTATACCTTTTGAAATTCAGCCTTTATGAGAAAGCTGTACTATCTTGTACCTGCTG 848

QY 421 CAGGGCTGCTGCTCAGATGTGGTGGAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 480

DB 849 CAGGGCTGCTGCTCAGATGTGGTGGAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 908

QY 481 GCCACATGATACATCTAAGAATTGTAACCTGTAATAAAAAAATGTTCCCTAACTGG 535

DB 909 GCCACATGATACATCTAAGAATTGTAACCTGTAATAAAAAAATGTTCCCTAACTGG 963

RESULT 2

AC132933

LOCUS

DEFINITION Mus musculus clone RP24-128D9, WORKING DRAFT SEQUENCE, 25 unordered pieces.

AC132933

VERSION AC132933.3 GI:28460829

KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 180007)

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE Mus musculus, clone RP24-128D9

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 180007)

AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 180007)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## COMMENT

Submitted (21-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Feb 21, 2003 this sequence version replaced gi:28269618.

All repeats were identified using RepeatMasker:

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L27253

Center clone name: L28\_D\_9

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 174258 bases at least Q40

Consensus quality: 175884 bases at least Q30

Consensus quality: 176691 bases at least Q20

Insert size: 177607; sum-of-contigs

Quality coverage: 10.8 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 25 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 33601: contig of 33601 bp in length  
\* 33602 33701: gap of 100 bp  
\* 33702 34361: contig of 660 bp in length  
\* 34362 34461: gap of 100 bp  
\* 34462 35133: contig of 672 bp in length  
\* 35134 35233: gap of 100 bp  
\* 35234 35962: contig of 729 bp in length  
\* 35963 36062: gap of 100 bp  
\* 36063 36782: contig of 720 bp in length

36783 36882: gap of 100 bp  
\* 36883 37333: contig of 451 bp in length  
\* 37334 37433: gap of 100 bp  
\* 37434 38130: contig of 697 bp in length  
\* 38131 38230: gap of 100 bp  
\* 38231 38939: contig of 709 bp in length  
\* 38940 39039: gap of 100 bp  
\* 39040 40065: contig of 1026 bp in length  
\* 40066 40165: gap of 100 bp  
\* 40166 40892: contig of 727 bp in length  
\* 40893 40992: gap of 100 bp  
\* 40993 41629: contig of 637 bp in length  
\* 41630 41729: gap of 100 bp  
\* 41730 42426: contig of 697 bp in length  
\* 42427 42526: gap of 100 bp  
\* 42527 43212: contig of 686 bp in length  
\* 43213 43312: gap of 100 bp  
\* 43313 43999: contig of 687 bp in length  
\* 44000 44099: gap of 100 bp  
\* 44100 44807: contig of 708 bp in length  
\* 44808 44907: gap of 100 bp  
\* 44908 45766: contig of 859 bp in length  
\* 45767 45866: gap of 100 bp  
\* 45867 49123: contig of 3257 bp in length  
\* 49124 49223: gap of 100 bp  
\* 49224 51352: contig of 2129 bp in length  
\* 51353 51452: gap of 100 bp  
\* 51453 59543: contig of 8091 bp in length  
\* 59544 59643: gap of 100 bp  
\* 59644 66930: contig of 7287 bp in length  
\* 66931 67030: gap of 100 bp  
\* 67031 78511: contig of 11481 bp in length  
\* 78512 78611: gap of 100 bp  
\* 78612 92092: contig of 13481 bp in length  
\* 92093 92192: gap of 100 bp  
\* 92193 113443: contig of 21251 bp in length  
\* 113444 113543: gap of 100 bp  
\* 113544 153243: contig of 39700 bp in length  
\* 153244 153343: gap of 100 bp  
\* 153344 180007: contig of 26664 bp in length.

## FEATURES

## Source

1. 180007  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="RP24-128D9"  
/clone\_lib="RPCI-24 Male Mouse BAC"  
1. 33601  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:left  
33702..34361  
/note="assembly\_fragment"  
34462..35133  
/note="assembly\_fragment"  
35234..35962  
/note="assembly\_fragment"  
36063..36782  
/note="assembly\_fragment"  
36883..37333  
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37434..38130  
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38231..38939  
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39040..40065  
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40166..40892  
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40993..41629  
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41730..42426  
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## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature

## misc\_feature



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	/note="assembly_fragment"													
misc_feature	43313..43999													
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misc_feature	44100..44807													
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misc_feature	44908..45766													
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misc_feature	45867..49123													
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misc_feature	49224..51352													
	/note="assembly_fragment"													
misc_feature	51453..59543													
	/note="assembly_fragment"													
misc_feature	59644..66930													
	/note="assembly_fragment"													
misc_feature	67031..78511													
	/note="assembly_fragment"													
misc_feature	78612..92092													
	/note="assembly_fragment"													
misc_feature	92193..113443													
	/note="assembly_fragment"													
misc_feature	113544..153243													
	/note="assembly_fragment"													
misc_feature	153344..180007													
	/note="assembly_fragment"													
	clone end:T7													
	vector_side:right"													
Query Match 97.5%; Score 521.4; DB 2; Length 180007;														
Best Local Similarity 99.6%; Pred. No. 4.8e-156;														
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;														
Qy	1	GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGTGGCTTACTGCCTG	60											
Db	173707	GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGTGGCTTACTGCCTG	173766											
Qy	61	GCAGGGACCGAGTACCACCTGAAATACCTCTTCTTCCCTCCATTTATGTGAGAAGGAC	120											
Db	173767	GCAGGGACCGAGTACCACCTGAAATACCTCTTCTTCCCTCCATTTATGTGAGAAGGAC	173826											
Qy	121	TCTCCCAAGTCAATTGACAGGCTCACATGTCCCTTTGCACATGGAACGCACTTCACTT	180											
Db	173827	TCTCCCAAGTCAATTGACAGGCTCACATGTCCCTTTGCACATGGAACGCACTTCACTT	173886											
Qy	181	TCAGTGATCACCACAGCATGCAATTTGTGCAGGAGAGTCACCGGAGGCCAAGTGCTAAA	240											
Db	173887	TCAGTGATCACCACAGCATGCAATTTGTGCAGGAGAGTCACCGGAGGCCAAGTGCTAAA	173946											
Qy	241	GCCACCTGCGTTTGCTTTCTCCTTCCATTGAGGAACTCACAACATGAGCCTGTGGAGTT	300											
Db	173947	GCCACCTGCGTTTGCTTTCTCCTTCCATTGAGGAACTCACAACATGAGCCTGTGGAGTT	174006											
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RESULT 3  
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LOCUS AC139212 203000 bp DNA linear HTG 04-MAR-2003

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus chromosome 16 clone RP23-331D17 map 16, WORKING DRAFT  
SEQUENCE, 8 unordered pieces.  
AC139212  
AC139212.3 GI:28828000  
HTG; HTGS PHASE1; HTGS DRAFT.  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Birren,B., Nusbaum,C. and Lander,E.  
Mus musculus chromosome 16, clone RP23-331D17  
Unpublished  
2 (bases 1 to 203000)  
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,  
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,  
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,  
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
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Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,  
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,  
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Direct Submission  
Submitted (27-JAN-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 203000)  
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,  
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,  
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,  
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,  
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Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL  
COMMENT

Direct Submission  
Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 4, 2003 this sequence version replaced gi:28630048.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L29145  
Center clone name: 331\_D\_17

----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 201586 bases at least Q40  
Consensus quality: 201837 bases at least Q30  
Consensus quality: 202010 bases at least Q20  
Insert size: 205000; agarose-fp  
Insert size: 202300; sum-of-contigs  
Quality coverage: 11.6 in Q20 bases; agarose-fp  
Quality coverage: 11.8 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1. 52046: contig of 52046 bp in length  
\* 52047 52146: gap of 100 bp  
\* 52147 53208: contig of 1062 bp in length  
\* 53209 53308: gap of 100 bp  
\* 53309 54451: contig of 1143 bp in length  
\* 54452 54551: gap of 100 bp  
\* 54552 56935: contig of 2384 bp in length  
\* 56936 57035: gap of 100 bp  
\* 57036 59943: contig of 2908 bp in length  
\* 59944 60043: gap of 100 bp  
\* 60044 85051: contig of 25008 bp in length  
\* 85052 85151: gap of 100 bp  
\* 85152 163137: contig of 77986 bp in length  
\* 163138 163237: gap of 100 bp  
\* 163238 203000: contig of 39763 bp in length.

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Best Local Similarity 99.6%; Pred. No. 4.9e-156;  
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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RESULT 4

AF166097  
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DEFINITION Mus musculus group X secreted phospholipase A2 (Pla2g10) mRNA, complete cds.  
ACCESSION AF166097  
VERSION AF166097.2 GI:5525307  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 1040)  
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.  
TITLE On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II enzymes  
JOURNAL J. Biol. Chem. 274 (44), 31195-31202 (1999)  
MEDLINE 20002639  
PUBMED 10531313  
REFERENCE 2 (bases 1 to 1040)  
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.  
TITLE Direct Submission  
JOURNAL Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France  
REFERENCE 3 (bases 1 to 1040)  
AUTHORS Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.  
TITLE Direct Submission  
JOURNAL Submitted (06-DEC-1999) IPMC, CNRS, 660, route des Lucioles, Valbonne 06560, France  
REMARK Sequence update by submitter  
COMMENT On Dec 6, 1999 this sequence version replaced gi:6164695.  
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BASE COUNT 244 a 258 c 277 g 261 t  
ORIGIN

Query Match 96.4%; Score 515.8; DB 10; Length 1040;  
Best Local Similarity 99.4%; Pred. No. 1.4e-154;  
Matches 528; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
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Db 493 GCAGAGAACAAATGCCAAGAACTTTTGTGACAGGTGTGACGAGGAGCTGGCTTACTGCCTG 552  
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RESULT 5  
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LOCUS BD095993 1040 bp .DNA linear PAT 27-AUG-2002  
DEFINITION Immunoassay for group X phospholipase A2.  
ACCESSION BD095993  
VERSION BD095993.1 GI:22641581  
KEYWORDS WO 0190195-A/10.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1040)  
REFERENCE Hanasaki, K., Imagawa, K. and Masuta, K.  
AUTHORS Immunoassay for group X phospholipase A2  
TITLE Patent: WO 0190195-A 10 29-NOV-2001;  
JOURNAL SHIONOGI & CO LTD, KOJI HANASAKI, KEIICHI IMAGAWA, KEIICHI MASUTA

COMMENT OS Mus musculus (mouse)  
PN WO 0190195-A/10  
PD 29-NOV-2001  
PF 21-NOV-2000 WO 2000JP008198  
PR 24-MAY-2000 JP 00P 152967  
PI KOJI HANASAKI, KEIICHI IMAGAWA, KEIICHI MASUTA  
PC C07K16/40, A61K39/395, A61P43/00, G01N33/53, G01N33/573, G01N33/574  
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FH Key Location/Qualifiers  
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Best Local Similarity 99.2%; Pred. No. 4.5e-154;  
Matches 527; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 GCAGAGAACAAATGCCAAGAACTTTTGTGACAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60  
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RESULT 6  
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LOCUS BD103482 1040 bp DNA linear PAT 27-AUG-2002  
DEFINITION Immunoassay for group X phospholipase A2.  
ACCESSION BD103482  
VERSION BD103482.1 GI:22649056  
KEYWORDS WO 0190196-A/10.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1040)  
REFERENCE Hanasaki, K., Imagawa, K. and Masuta, K.  
AUTHORS Immunoassay for group X phospholipase A2  
TITLE



JOURNAL Patent: WO 0190196-A 10 29-NOV-2001; SHIONOGI & CO LTD,KOJI HANASAKI,KEIICHI IMAGAWA,KEIICHI MASUTA  
COMMENT OS Mus musculus (mouse)  
PN WO 0190196-A/10  
PD 29-NOV-2001  
PF 22-MAY-2001 WO 2001JP0004267  
PR 24-MAY-2000 JP OOP 152967,21-NOV-2000 WO PCTJP0008198 PI KOJI HANASAKI,KEIICHI IMAGAWA,KEIICHI MASUTA  
PC C07K16/40,C12N9/16,C12P21/08,A61K39/395,G01N33/53,G01N33/574,  
PC G01N33/576  
CC Immunoassay for group X phospholipase A2  
FH Key Location/Qualifiers  
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Query Match 96.1%; Score 514.2; DB 6; Length 1040;  
Best Local Similarity 99.2%; Pred. No. 4.5e-154;  
Matches 527; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 GCAGAGACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGTGGCTTACTGCGCTG 60  
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493 GCAGAGACAGATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGTGGCTTACTGCGCTG 552  
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DEFINITION Mus musculus clone RP23-26110, WORKING DRAFT SEQUENCE, 7 unordered pieces.  
ACCESSION AC120860  
VERSION AC120860.3 GI:28876105  
KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 185784)  
Birren,B., Nusbaum,C. and Lander,E.  
Mus musculus, clone RP23-26110  
Unpublished  
2 (bases 1 to 185784)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,  
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,  
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,  
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,  
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,  
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,  
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,  
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,  
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,  
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,  
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 185784)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,  
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,  
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,  
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,  
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,  
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL  
COMMENT

Submitted (07-MAR-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 7, 2003 this sequence version replaced gi:28195444.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L22304  
Center clone name: 26\_I\_10  
----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 183652 bases at least Q40  
Consensus quality: 184566 bases at least Q30







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misc\_feature 10669..11530  
/note="assembly\_fragment"  
misc\_feature 11631..12340  
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Best Local Similarity 87.2%; Pred. No. 6.9e-100;  
Matches 441; Conservative 0; Mismatches 53; Indels 12; Gaps 5;

Qy 24 TTTGTGCGAGTGTGACGAGGAGCTGGCTTACTGCTGGCAGGACCGAGTACCACCTGAA 83  
Db 186234 TGTGTGCGAGTGTGACGAGGAGCTGGCTTACTGCTGGCAGCAACCGAGTACCACCTGGAG 186293

Qy 84 ATACCTCTTCTCCCTCCATTTATGTGAGAGGAGCTCTCCCAAGTGAATTGACAGGC 143  
Db 186294 ATACTTCTTCTCCCTCTATTATTATGTGAGAGAGACTCACCCAAAGTGGAGTGCAGGC 186353

Qy 144 TCACATGTCCTTTGACATGGAACGCACTTCACTTTCACTGATCAACCAACAGCATGCA 203  
Db 186354 T-ACATGTCCTTTACACATGGAATGCAATGCGCTTTCAGTCAAT-----GCAGCATGCA 186407

Qy 204 ATTTGTGCGAGAGTACACCGGAGGCAAGTCTAAAGCCACCTGCGTTTGTCTTCTCCT 263  
Db 186408 ATTTATGCATAAGAAATCCCTGGAGGCAAGTCAACAG---CCTGCATTTGCTTCTCCC 186464

Qy 264 TCCATTGAGGAAGTCACTGAGGCTGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 323  
Db 186465 TCCATTGAGGAAGTCACTGAGGCTGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 186524

Qy 324 TCCTGGGCTGTTTATACAAATAGCGCTGTTGTTGGGCTGGTGGTGGTGGTGGTGGTGGTGG 441  
Db 186525 TCCTGGGCTGTTTATACAAATAGCGCTGTTGTTGGGCTGGTGGTGGTGGTGGTGGTGGTGG 383

Qy 384 AGCCTTTATGAGAGAGTGTACTATCTTGTACCTGCTGC--AGGGCTGCTGGTGCAGATGTG 441  
Db 186584 AACCTTTATGAGAGAGTGTACTATCTTGTACCTGCTGCAGAGGTTGGTGGTGGTGGTGGTGG 186643

Qy 442 GGTGAACACCTGCTTAGGCTTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 501  
Db 186644 GATGAACACCTGCTTAGGCTTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 186703

Qy 502 TTGTAACCTGTAATAAAAAATGTTCC 527  
Db 186704 TTGTAACCTGTAATAAAAAATGTTCC 186729

RESULT 9  
AF166100 910 bp mRNA linear ROD 31-OCT-1999  
LOCUS  
DEFINITION  
Rattus norvegicus group X secreted phospholipase A2 mRNA, complete cds.  
ACCESSION  
AF166100  
VERSION  
AF166100.1 GI:6164701  
KEYWORDS  
Rattus norvegicus (Norway rat)  
SOURCE  
ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
1 (bases 1 to 910)  
AUTHORS  
Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.  
TITLE  
On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II enzymes  
J. Biol. Chem. 274 (44), 31195-31202 (1999)  
JOURNAL  
MEDLINE  
20002639  
PUBMED  
10531313  
REFERENCE  
2 (bases 1 to 910)  
AUTHORS  
Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles,

Valbonne 06560, France  
Location/Qualifiers  
1..910  
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/codon\_start=1  
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BASE COUNT 224 a 216 c 235 g 235 t

ORIGIN

Query Match 55.4%; Score 296.2; DB 10; Length 910;  
Best Local Similarity 80.3%; Pred. No. 8.2e-84;  
Matches 425; Conservative 0; Mismatches 88; Indels 16; Gaps 6;

Qy 1 GCAGAGAACAAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60  
Db 367 GCAGAGAACAAATGCCAAGAACTCCTATGAGGTGTGATGAGACGCTCGCATACTGCCTG 426

Qy 61 GCAGGACCGAGTACCACTGAAATACCTCTTCTTCCCTCCATTTATGTGAGAAAGGAC 120  
Db 427 GCAGACACAGAGTACCACTGAAATACCTCTTCTTCCCTCGGTTTATGTGAGAAAGGAC 486

Qy 121 TCTCCCAAGTCAATTTGACAGGCTCACATGTCCCTTTGCACATGGAACGCACCTTCACTT 180  
Db 487 TCACCAAGTGCAACTAATAGGTGAAATGTCCCTTTGCACATGGAATGAAGTTCGCTT 546

Qy 181 TCAGTGATCAACCAACAGCATGCAATTTGTGAGGAGAGTACCGAGGCAAGTCTAAA 240  
Db 547 TCAGTGATCAACCAACAGCATGCAATTTGTGAGGAGAGTACCGAGGCAAGTCTAAA 604

Qy 241 GCCACCTGCTTTGCTTCTCTCCCTCCATTCAGGAACCTCACAACCTATGAGCCTGTGGAGTT 300  
Db 605 G---CCTGGGTTGCTTCTCTCCCTCCATTCGTGAACCTCAGGACTATGAGCCTGTGGAGCT 661

Qy 301 GCCAGTCTGATGAAGGTTCAAAGTCTGGGCTGTTTATACAAATAAGCGCTGTGTTGG 360  
Db 662 GCCAGTCTGATGAAGGTTGAGAGTCTGGGCTGTTTATACAAATAAGCGCTGTGTTGG 720

Qy 361 GCGTGTATATCTTTTGAAATTCAGCCTTTATGAGAAAGCTGTACTATCTTGTACCTGCTG 420  
Db 721 GCTTGATATAATTTTGAAGTCCAACTTTACAAAAGCTTTACTACTGTGTAACTGCTG 780

Qy 421 C--AGGCTGCTGGTGCAGATGTGGGTGAACACCTGCTTAGGCTTTGCTGTGGTAATAACA 478  
Db 781 CAGAGGTTGGTGGTCAAA-----TGAACACCTGCTTAGGCTTGTGGTGTGGTAATAACA 834

Qy 479 TTGCCACATGATACATCTAAGAAATGTAAGTGTAAATAAAAAATGTTCC 527  
Db 835 TTGCCAC--GATACATCTAGGAATGTTAGTGTAAATAAGCATGTTCCC 881

RESULT 10  
AC128180  
LOCUS  
DEFINITION  
Rattus norvegicus clone CH230-373N16, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 11 unordered pieces.  
ACCESSION  
AC128180  
VERSION  
AC128180.2 GI:23908197  
KEYWORDS  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
SOURCE  
Rattus norvegicus (Norway rat)  
ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
1 (bases 1 to 332220)



AUTHORS

Muzny,D,Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falles,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,B., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,B., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE

JOURNAL

Unpublished

2 (bases 1 to 332220)

Worley,K.C.

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

AUTHORS

TITLE

JOURNAL

3 (bases 1 to 332220)

Rat Genome Sequencing Consortium.

Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Oct 12, 2002 this sequence version replaced gi:21908782. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GZNT

Center clone name: CH230-373N16

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 210811 bases at least Q40

Consensus quality: 214286 bases at least Q30

Consensus quality: 216531 bases at least Q20

Estimated insert size: 223402; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 11 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 60608: contig of 60608 bp in length

\* 60609 60708: gap of unknown length

\* 60709 65888: contig of 5180 bp in length

\* 65889 65988: gap of unknown length

\* 65989 98233: contig of 32245 bp in length

\* 98234 98333: gap of unknown length

\* 98334 103602: contig of 5269 bp in length

\* 103603 103702: gap of unknown length

\* 103703 123008: contig of 19306 bp in length

\* 123009 123108: gap of unknown length

\* 123109 308819: contig of 185711 bp in length

\* 308820 308919: gap of unknown length

\* 308920 320683: contig of 11764 bp in length

\* 320684 320783: gap of unknown length

\* 320784 322464: contig of 1681 bp in length

\* 322465 322564: gap of unknown length

\* 322565 324598: contig of 2034 bp in length

\* 324599 324698: gap of unknown length

\* 324699 326126: contig of 1428 bp in length

\* 326127 326226: gap of unknown length

\* 326227 332220: contig of 5994 bp in length.

FEATURES

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/db\_xref="taxon:10116"

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/note="clone boundary

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site:MboI

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/note="wgs\_contig"

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/note="wgs\_contig"

116648..117691

/note="wgs\_contig"

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clone end:T7"
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/note="wgs end_extension
clone end:T7"
BASE COUNT 64872 a 48021 c 47726 g 57171 t 114430 others
ORIGIN
Query Match 55.4%; Score 296.2; DB 2; Length 332220;
Best Local Similarity 79.1%; Pred. No. 2.1e-83;
Matches 417; Conservative 0; Mismatches 98; Indels 12; Gaps 5;
QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGCTGGTTACTGCCTG 60
Db 282163 GCAGAGAACAAATGCCAAGAACTCTATGCGAGGTGTGATGAGACGCTCGCATACTGCCTG 282222
QY 61 GCAGGGACCGAGTACCACTGAAATACCTTTCTTCCCTCCCTCCATTTTATGTGAGAAAGGAC 120
Db 282223 GCAGACACAGAGTACCACTGAAATACCTTTCTTCCCTCCCTCGGTTTATGTGAGAAAGGAC 282282
QY 121 TCTCCCAAGTGCAATGTACAGGCTCACATGTCCTTTGCACATGGAAACGCACTTCACCTT 180
Db 282283 TCACCCCAAGTGCAACTAATAGGTGAAATGTCCCTTTGCACATGGAAATGAAGTTCGCTT 282342
QY 181 TCAGTGTATCACCAACAGCATGCAATTTGTGCGAGAGAGTCAACGGAGGCCAAGTGCTAAA 240
Db 282343 TCAGTGTATGAACAACAGACCTTCGATTTGCGCAG--GAGTCCCTGGAGGCCAAGTGATGAA 282400
QY 241 GCCACCTGCGTTTGTCTTCTCCTTCCATTCAGGAACTCACAACATATGAGCCTGTGGAGTT 300
Db 282401 G---CCTGGGTTTGTCTTCTCCTCCTCATTCGTGAACTCAGGACTATGAGCCTGTGGAGCT 282457
QY 301 GCCAGTCTGATGAAGGTTCAAAGTCTCGGCTGTTTATACAAATAAGCGCTGTGTGG 360
Db 282458 GCCAGTTTGTATGAAGGTTGAGAGTCTCTGGGCTGTTTATACAACCT-GCAACTGTGTGG 282516
QY 361 GCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAACTGTACTATCTTGTACCTGCTG 420
Db 282517 GCTTGATATAATTTTGAAGTCCAACCTTTACAAAAGCTTTACTACTGTGTAACTGCTG 282576
QY 421 CAGGGCTGCTGGTCAAGATGTGGTGAACACCTGCTTAGGCTTTGCTGTGTAATAACATT 480
Db 282577 CAGAG---GGTTGGTGTCAAATGAACACCTGCTTAGGCTTGTGTTGGTAATAACATT 282632
QY 481 GCCACATGATACATCTAAGAATTGTAAGTGTAAATAAAAAAATGTTCC 527
Db 282633 GCCAC--GATACATCTAGGAATTGTTAGTGTAAATAAAGCATGTTCCC 282677
RESULT 11
AC133544/c 86186 bp DNA linear HTG 14-SEP-2002
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-115C1, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
AC133544
AC133544.1 GI:22857540
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 86186)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 86186)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 450574
Center clone name: RPCI-11_115C1
-----
Summary Statistics
Consensus quality: 84676 bases at least Q40
Consensus quality: 85119 bases at least Q30
Consensus quality: 85392 bases at least Q20
Estimated insert size: 110000; agarose-fp estimation
Estimated insert size: 85786; sum-of-contigs estimation
Quality coverage: 14.87 in Q20 bases; agarose-fp estimation
Quality coverage: 19.07 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1138: contig of 1138 bp in length
* 1139 1238: gap of unknown length
* 1239 7458: contig of 6220 bp in length
* 7459 7558: gap of unknown length
* 7559 23435: contig of 15877 bp in length
* 23436 23535: gap of unknown length
* 23536 36643: contig of 13108 bp in length
* 36644 36743: gap of unknown length
* 36744 86186: contig of 49443 bp in length.
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="16"
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/clone_lib="RPCI human BAC library 11"
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Query Match 27.3%; Score 146.2; DB 2; Length 86186;
Best Local Similarity 66.0%; Pred. No. 3.7e-35;
Matches 315; Conservative 0; Mismatches 133; Indels 29; Gaps 6;
QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCGAGGTGTGACGAGGAGCTGGTACTGCCTG 60
Db 48365 GCAGAGAACAAATGCCAAGAACTGTGTGCAAGTGTGACCGAGGATGCTTA 48306
QY 61 GCAGGGACCGAGTACCACTGAAATACCTTCTTCCCTCCCTCATTTTATGTGAGAAAGGAC 120
Db 48305 GCCCAAACTGAGTACAACTTAAAGTACCTTCTTACCCCCAGTTCTCTATGTGAGCGGAC 48246
QY 121 TCTCCCAAGTGAATGACAGGC-----TCACATGTCCTTTCACATGGAAGGCACT 174
Db 48245 TCGCCCAAGTGTGACTGACTACCTTGACTTGAATGCTCTTTTGCACAGGAATAAGC 48186
```





JOURNAL Submitted (25-FEB-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT -----Genome Center Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov

----- Project Information Center Project Name: 452911 Center clone name: RPCI-11\_121D10

----- Summary Statistics Consensus quality: 114212 bases at least Q40 Consensus quality: 114858 bases at least Q30 Consensus quality: 115531 bases at least Q20 Estimated insert size: 175000; agarose-fp estimation Estimated insert size: 116974; sum-of-contigs estimation Quality coverage: 13.07 in Q20 bases; agarose-fp estimation Quality coverage: 19.56 in Q20 bases; sum-of-contigs estimation

\* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 1159: contig of 1159 bp in length \* 1160 1259: gap of unknown length \* 1260 2760: contig of 1501 bp in length \* 2761 2860: gap of unknown length \* 2861 7171: contig of 4311 bp in length \* 7172 7271: gap of unknown length \* 7272 11692: contig of 4421 bp in length \* 11693 11792: gap of unknown length \* 11793 18058: contig of 6266 bp in length \* 18059 18158: gap of unknown length \* 18159 24831: contig of 6673 bp in length \* 24832 24931: gap of unknown length \* 24932 53782: contig of 28851 bp in length \* 53783 53882: gap of unknown length \* 53883 93841: contig of 39959 bp in length \* 93842 93941: gap of unknown length \* 93942 117774: contig of 23833 bp in length.

FEATURES Location/Qualifiers source 1. 117774 /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" /chromosome="16" /clone="RP11-121D10" /clone\_lib="RPCI human BAC library 11" /base\_count 30315 a 27527 c 27197 g 31935 t 800 others

BASE COUNT 30315 a 27527 c 27197 g 31935 t 800 others ORIGIN

Query Match 27.3%; Score 146.2; DB 2; Length 117774; Best Local Similarity 66.0%; Pred. No. 3.9e-35; Matches 315; Conservative 0; Mismatches 133; Indels 29; Gaps 6;

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QY 61 GCAGGACCGAGTACCACTGAAATACCTCTTCTCCCTCCATTTTATGTGAGAGGAC 120 |||||||

Db 41262 GCCCAAACTGAGTACAACTTAAAGTACCTCTTCTACCCCACTTCCTATGTGAGCCGAC 41321 |||||||

QY 121 TCTCCCAAGTGCAATGACAGGC-----TCACATGTCCTTTGCACATGGAACGCACT 174 |||||||

Db 41322 TCGCCCAAGTGTGACTGACTGACTTACCTTGACTTGAATGCTCTTTTGCACAGGAATAAAGC 41381 |||||||

QY 175 TCACCTTTCACTGATCACCACAGCATGCAATTTGTGCAGGAGAGTCAACCGAGGCCAAGT 234 |||||||

Db 41382 GTCCTCTCAGTAATGAACAACAGCATTCAAGTTATTTCGAGA-AGGGAACCGAAGCCAACT 41440

QY 235 GCTAAAGCCA-----CCTGCGTTTGTCTTCTCCTTCATTCCATTCAGGAACCTCAACAATGAGC 290 |||||||

Db 41441 GATAAAGCCACAACTTGTGTGCTTTCCCTCCCAATCCAGAACTCAGGACTGGAGCC 41500 |||||||

QY 291 CTGTGGAGTTGCCAGTCTGATGAAGGTTCAAAGTCTCGGCCCTGTTTATACAAATA-- 347 |||||||

Db 41501 CATGTGGTTTG-----CAGTTAAAGGCCAAAGTCTCGCACCTATTTTATAAACTATGA 41555 |||||||

QY 348 -----AGCGCTGTGTGGCGTGGTATACATTTTCAAAATTCAGCCTTTATGAGAGC 399 |||||||

Db 41556 CTGTGTTTATCACTGTGTGGGTGGTTCATTTTTCAGGTTCATCTTTATGAAAAGA 41615 |||||||

QY 400 TGTACTATCTTGTA--CCTGCTGCAGGGCTGCTGCTCAGATGTGGTGAACACCTGC 454 |||||||

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RESULT 14 AC009167 193633 bp DNA linear PRI 18-MAR-2003

LOCUS AC009167 Homo sapiens chromosome 16 clone RP11-82018, complete sequence.

DEFINITION AC009167

ACCESSION AC009167

VERSION AC009167.9 GI:29029222

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 193633) DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

AUTHORS Direct Submission

TITLE Unpublished

JOURNAL 2 (bases 1 to 193633) DOE Joint Genome Institute.

REFERENCE 2 Direct Submission

AUTHORS Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

TITLE 3 (bases 1 to 193633) DOE Joint Genome Institute.

JOURNAL Direct Submission

REFERENCE 3 Submitted (04-DEC-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

AUTHORS 4 (bases 1 to 193633) DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

TITLE Direct Submission

JOURNAL Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Mar 18, 2003 this sequence version replaced gi:17298590. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory www.shgc.stanford.edu

Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.

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QY 121 TCTCCCAAGTGAATGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174  
Dd |||||  
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QY 175 TCACCTTTTCAGTGATCACCACAGCATGCAATTTGTGAGGAGAGTCAACGGAGGCCAAGT 234  
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49267 GTCCTCTCAGTAATGAACAACAGCATTCAGTTATTGCGAGA-AGGGAACCGAAGCCAAAGT 49325  
QY 235 GCTAAAGCCA-----CCTGCGTTTGTCTTCTCTCCCTCCATTCAGGAACCTCACAACATATGAGC 290  
Dd |||||  
49326 GATAAAGCCACAACCTTGTGTTGCTTCTCCCTCCCAATCCAGAACTCAGGACTGGAGCC 49385  
QY 291 CTGTGGAGTTCAGTCTGATGAAGTTCAAGTCTGGGCTCTGTTTATACAAATA--- 347  
Dd |||||  
49386 CATGTGGTTG-----CAGTTAAAGGCCAAAGTCTGCACCTATTTTATAAAACTATGA 49440  
QY 348 -----AGCGTGTGTTGGCGTGTATACCTTTTGAATTCAGCCTTATGAGAAAGC 399  
Dd |||||  
49441 CTGTGTTTATCACTGTGTTGGGTCGTTCCATTTTGAGGTTCCATCTTTATGAAAGA 49500  
QY 400 TGTACTATCTTGTGA--CCTGCTGCAGGCTGTGCTGATGTGGTGGAACACCTGC 454  
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49501 TAACCTGTCTTCAACCTGCTTGGATGGCTGTAGTCAATGTGAACGAAACCTAC 49557

RESULT 15  
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DEFINITION Gorilla gorilla gorilla clone CH255-165B15, WORKING DRAFT SEQUENCE,  
14 unordered pieces.  
AC145040  
AC145040.1 GI:31376426  
VERSION HTG; HTGS PHASE1; HTGS DRAFT.  
KEYWORDS Gorilla gorilla gorilla (lowland gorilla)  
SOURCE Gorilla gorilla gorilla  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
REFERENCE 1 (bases 1 to 198276)  
AUTHORS Eichler,E.E., Johnson,M.E., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,B.H., Masiello,C., Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
REFERENCE 2 (bases 1 to 198276)  
AUTHORS Green,E.D.  
TITLE Direct Submission  
JOURNAL Submitted (04-JUN-2003) NIH Intramural Sequencing Center, 8717  
REFERENCE Groveomont Circle, Gaithersburg, MD 20877, USA  
AUTHORS ----- Genome Center  
TITLE Center: NIH Intramural Sequencing Center  
JOURNAL Center code: NISC  
AUTHORS Web site: http://www.nisc.nih.gov  
TITLE Contact: nisc\_zoo@nhgri.nih.gov  
JOURNAL ----- Project Information  
REFERENCE Center project name: enl  
AUTHORS Center clone name: 165B15  
TITLE ----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 194149 bases at least Q40  
Consensus quality: 195069 bases at least Q30  
Consensus quality: 195474 bases at least Q20  
Insert size: 155000; agarose-fp  
Insert size: 196976; sum-of-contigs  
Quality coverage: 11.60x in Q20 bases; agarose-fp  
Quality coverage: 9.13x in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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\* 10463 10562: gap of unknown length  
\* 10563 16903: contig of 6341 bp in length  
\* 16904 17003: gap of unknown length  
\* 17004 23921: contig of 6918 bp in length  
\* 23922 24021: gap of unknown length  
\* 24022 28475: contig of 4454 bp in length  
\* 28476 28575: gap of unknown length  
\* 28576 39752: contig of 11177 bp in length  
\* 39753 39852: gap of unknown length  
\* 39853 50370: contig of 10518 bp in length  
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\* 50471 69020: contig of 18550 bp in length  
\* 69021 69120: gap of unknown length  
\* 69121 86310: contig of 17190 bp in length  
\* 86311 86410: gap of unknown length  
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\* 114284 114383: gap of unknown length  
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Best Local Similarity 66.0%; Pred. No. 4.3e-35;
Matches 315; Conservative 0; Mismatches 133; Indels 29; Gaps 6;

QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGTGGCTTACTGCCTG 60
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QY 61 GCAGGGACCGAGTACCACCTGAAATACCTCTTCTCCCTCCATTTTATGTGAGAGGAC 120
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QY 121 TCTCCCAAGTGCAATTGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174
Db 73893 TCGCCCAAGTGTGACTGACTACCTTGACTTGAATGCTTTTGTGCACAGGAAATAAAC 73952

QY 175 TCACCTTTCAGTGATCACCAACAGCATGCAATTTGTGCAGGAGAGTCACCGGAGGCCAAGT 234
Db 73953 GTCCTCTCAGTAAATGAACAACAGCATTCAGTTATTTGCAGA-AGGGAACCGAAGCCAAGT 74011

QY 235 GCTAAAGCCA-----CCTGCGTTTGTCTTCTCCTCCATTTCAGGAACCTCAAACTATGAGC 290
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QY 291 CTGTGGAGTTGCCAGTCTGATGAAGGTTCAAAGTCTCTGGGCTGTTTATACAAATA--- 347
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QY 400 TGTAATCTTTGTA--CCTGCTGCAGGGCTGCTGCTCAGATGTGGGTGAACACCTGC 454
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Job time : 2134 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:39:44 ; Search time 256 Seconds  
(without alignments)  
5641.404 Million cell updates/sec

Title: US-09-620-607B-34  
Perfect score: 535  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514.2	96.1	1040	ABL58680	Mouse X-type secre
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3	120	22.4	742	AAX79001	Human phospholipas
4	119.2	22.3	1737	AAS91740	DNA encoding novel
5	95.2	17.8	1020	ABL58671	Human secretory ph
6	95.2	17.8	1020	ABA96621	Human X-type secre
c	94	17.6	445	ABL61868	Colon adenocarcino
c	94	17.6	445	ABL67612	Oesophagus cancer

9	87.8	16.4	465	24	ABL58672	Human X-type secre
10	87.8	16.4	465	24	ABA96622	Human X-type secre
11	63.4	11.9	65	24	ABN57123	Mouse spliced tran
c	36	6.7	758	23	AAS67219	DNA encoding novel
c	36	6.7	758	23	AAS84693	DNA encoding novel
c	35.4	6.6	830	20	AAX33519	Human H19 promoter
c	35.4	6.6	830	21	AAA72969	Human H19 promoter
c	35.4	6.6	830	22	AAD21350	Human H19 promoter
c	35.4	6.6	3489	24	ABL62107	Colon adenocarcino
c	35.2	6.6	1830121	17	AAT42063	Haemophilus influe
19	34.6	6.5	709	21	AAC64439	Lycopersicon escul
20	34.6	6.5	709	21	AAC64449	Lycopersicon escul
c	33.8	6.3	833	20	AAX33520	Human H19 promoter
c	33.8	6.3	833	21	AAA72970	Human H19 promoter
c	33.8	6.3	833	22	AAD21351	Human H19 promoter
c	33.6	6.3	1204	24	ABK34913	Human cDNA encodin
c	33.6	6.3	26776	20	AAX20254	Borrelia burgdorfe
c	33.4	6.2	1925	17	AAT41945	ACC oxidase gene p
c	33.4	6.2	3681	20	AAX05593	Nucleotide sequenc
c	33	6.2	5971	23	AAS70348	DNA encoding novel
29	33	6.2	33718	22	AAK65257	Human immune/haema
30	33	6.2	33718	22	AAK86411	Human immune/haema
31	32.8	6.1	14041	22	AAH48024	Internal control B
32	32.6	6.1	6836	24	AAD45336	Human anti-microbi
33	32.6	6.1	659158	25	ABX16390	Mouse high growth
34	32.2	6.0	23580	22	AAS28556	Genomic sequence #
35	32.2	6.0	23580	22	AAK87248	Human immune/haema
36	32.2	6.0	86080	24	ABQ88164	Human osteoblast d
37	32.2	6.0	86080	24	ABK83561	Human cDNA differe
c	32.2	6.0	580073	18	AAT58840	Mycoplasma genital
c	31.8	5.9	3655	23	ABL10552	Drosophila melanog
40	31.8	5.9	6467	24	ABN80169	Human chemically m
c	31.8	5.9	7616	23	ABL26746	Drosophila melanog
42	31.6	5.9	562	22	AAK37355	Human bone marrow
43	31.6	5.9	562	24	ABS11341	Human genome-deriv
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45	31.6	5.9	1125	24	ABL68131	Ovary cancer relat

ALIGNMENTS

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AC ABL58680;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Mouse X-type secretory phospholipase A2 encoding sequence.  
XX  
KW Mouse; X-type secretory phospholipase A2; X-type sPLA2; cancer; colon;  
KW liver; lung; stomach; kidney; gallbladder; prostate; spleen; testis;  
KW ovary; Alzheimer's disease; hepatocirrhosis; immunoassay; gene; ds.  
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OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
CDS 175..630  
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FT /product= "mouse X-type secretory phospholipase A2"  
XX  
PN WO200190196-A1.  
XX  
PD 29-NOV-2001.  
XX  
PF 22-MAY-2001; 2001WO-JP04267.  
XX  
PR 24-MAY-2000; 2000JP-0152967.  
PR 21-NOV-2000; 2000WO-JP08198.  
XX  
PA (SHIO ) SHIONOGI & CO LTD.

XX PI Hanasaki K, Imagawa K, Masuta K;  
XX WPI; 2002-404351/43.  
DR P-PSDB; ABB80084.  
XX  
PT Immunoassay of X-type phospholipase A2 with antibody recognising part  
PT of it for quantitation of activated version, useful in diagnosis of  
PT e.g. cancer of colon, prostate, ovary or spleen, Alzheimer's disease  
PT and hepatocirrhosis  
XX  
PS Example 16; Page 53-54; 59pp; Japanese.  
XX  
CC The invention relates to an antibody that can specifically recognise a  
CC part of X-type secretory phospholipase A2 (X-type sPLA2). The immunoassay  
CC of the invention is used in the diagnosis of e.g. cancer of the colon,  
CC liver, lung, stomach, kidney, gallbladder, prostate, spleen, testis or  
CC ovary, Alzheimer's disease and hepatocirrhosis. The current sequence  
CC represents a mouse X-type secretory phospholipase A2 encoding sequence.  
XX  
SQ Sequence 1040 BP; 243 A; 258 C; 278 G; 261 T; 0 other;  
  
Query Match 96.1%; Score 514.2; DB 24; Length 1040;  
Best Local Similarity 99.2%; Pred. No. 6.6e-165;  
Matches 527; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
  
QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCGAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60  
DB |||||||  
493 GCAGAGAACAGATGCCAAGAACTTTTGTGCGAGGTGTGACGAGGAGCTGGCTTACTGCCTG 552  
  
QY 61 GCAGGGACCGAGTACCACTGAAATACCTTCTTCCCTCCATTTTATGTGAGAAGGAC 120  
DB |||||||  
553 GCAGGGACCGAGTACCACTGAAATACCTTCTTCCCTCCATTTTATGTGAGAAGGAC 612  
  
QY 121 TCTCCCAAGTGCAATTTGACAGGCTCACATGTCCTTTGCACATGGAACGCACCTTCACTT 180  
DB |||||||  
613 TCTCCCAAGTGCAATTTGACAGGCTCACATGTCCTTTGCACATGGAACGCACCTTCACTT 672  
  
QY 181 TCAGTGATCACCAACAGCATGCAATTTGTGCGAGGAGAGTACCGGAGGCCAAGTGCTAAA 240  
DB |||||||  
673 TCAGTGATCACCAACAGCATGCAATTTGTGCGAGGAGTACCGGAGTGCTAAA 732  
  
QY 241 GCCACCTGCGTTTGTCTTCTCCCTTCCATTGAGGAGTACCACTATGAGCCTGTGGAGTT 300  
DB |||||||  
733 GCCACCTGCGTTTGTCTTCTCCATTGAGGAGTACCACTATGAGCCTGTGGAGTT 792  
  
QY 301 GCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTTTATACAAATAGCGCTGTGTTGG 360  
DB |||||||  
793 GCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTTTATACAAAT-AGCGCTGTGTTGG 851  
  
QY 361 GCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAAGTGTACTATCTTGTACCTGCTG 420  
DB |||||||  
852 GCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAAGTGTACTATCTTGTACCTGCTG 911  
  
QY 421 CAGGGCTGCTGGTCAGATGTGGTGAAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 480  
DB |||||||  
912 CAGGGCTGCTGGTCAGATGTGGTGAAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 971  
  
QY 481 GCCACATGATACATCTAAGATTGTAACCTGTAATAAAAAAATGTTCCCTAA 531  
DB |||||||  
972 GCCACATGATACATCTAAGATTGTAACCTGTAATAAAAAAATGTTCCCTAA 1022  
  
RESULT 2  
ABA96630  
ID ABA96630 standard; cDNA; 1040 BP.  
XX  
AC ABA96630;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mouse X-type secretory phospholipase A2 (sPLA2) cDNA.  
XX

KW Mouse; murine; X-type; secretory phospholipase A2; sPLA2; immunoassay;  
KW cancer; tumour; colon; lung; liver; stomach; kidney; gall bladder;  
KW prostate; pancreas; Alzheimer's disease; liver cirrhosis; cytostatic;  
KW neutrotropic; neuroprotective; hepatotropic; gene; ss.  
XX  
OS Mus musculus.  
XX  
XX Key Location/Qualifiers  
FH CDS 175..630  
FT /\*tag= a  
FT /product= "Mouse X-type sPLA2"  
XX  
XX WO200190195-A1.  
XX  
XX 29-NOV-2001.  
XX  
XX 21-NOV-2000; 2000WO-JP08198.  
XX  
XX 24-MAY-2000; 2000JP-0152967.  
XX  
XX (SHIO ) SHIONOGI & CO LTD.  
XX  
XX Hanasaki K, Imagawa K, Masuta K;  
XX  
XX WPI; 2002-097648/13.  
DR P-PSDB; AAM49005.  
XX  
XX Antibodies recognizing parts of X-type phospholipase A2 and their use  
PT in immunoassays for diagnosis of cancer and Alzheimer's disease -  
XX  
XX Example 16; Page 46-47; 51pp; Japanese.  
PS  
XX  
XX The invention relates to antibodies which recognise parts of human X-type  
CC secretory phospholipase A2 (sPLA2; AAM49001, AAM49002). The antibodies of  
CC the invention are specific for the N-terminal propeptide sequence (Glu  
CC -11 to Arg -1) or for the active enzyme (Gly 1 to Asp 123). The invention  
CC also relates to a method of assaying for the X-type sPLA2 propeptide or  
CC active enzyme, and a method for the diagnosis of X-type sPLA2-associated  
CC diseases using the assay. The differing specificities of the antibodies  
CC allows determination of the relative amounts of proenzyme and active  
CC enzyme present. The invention also encompasses drug compositions which  
CC contain antibodies to the sPLA2 active enzyme for the treatment of  
CC X-type sPLA2-associated diseases. The antibodies are used for the  
CC diagnosis and treatment of X-type sPLA2-associated diseases including  
CC cancer of the colon, lung, liver, stomach, kidney, gall bladder, prostate  
CC and pancreas, Alzheimer's disease and liver cirrhosis. The present  
CC sequence is a cDNA encoding mouse X-type sPLA2 isolated in an  
CC exemplification of the invention.  
XX  
SQ Sequence 1040 BP; 243 A; 258 C; 278 G; 261 T; 0 other;  
  
Query Match 96.1%; Score 514.2; DB 24; Length 1040;  
Best Local Similarity 99.2%; Pred. No. 6.6e-165;  
Matches 527; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
  
QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCGAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60  
DB |||||||  
493 GCAGAGAACAGATGCCAAGAACTTTTGTGCGAGGTGTGACGAGGAGCTGGCTTACTGCCTG 552  
  
QY 61 GCAGGGACCGAGTACCACTGAAATACCTTCTTCCCTCCATTTTATGTGAGAAGGAC 120  
DB |||||||  
553 GCAGGGACCGAGTACCACTGAAATACCTTCTTCCCTCCATTTTATGTGAGAAGGAC 612  
  
QY 121 TCTCCCAAGTGCAATTTGACAGGCTCACATGTCCTTTGCACATGGAACGCACCTTCACTT 180  
DB |||||||  
613 TCTCCCAAGTGCAATTTGACAGGCTCACATGTCCTTTGCACATGGAACGCACCTTCACTT 672  
  
QY 181 TCAGTGATCACCAACAGCATGCAATTTGTGCGAGGAGAGTACCGGAGGCCAAGTGCTAAA 240  
DB |||||||  
673 TCAGTGATCACCAACAGCATGCAATTTGTGCGAGGAGTACCGGAGTGCTAAA 732  
  
QY 241 GCCACCTGCGTTTGTCTTCTCCCTTCCATTGAGGAGTACCACTATGAGCCTGTGGAGTT 300  
DB |||||||  
733 GCCACCTGCGTTTGTCTTCTCCATTGAGGAGTACCACTATGAGCCTGTGGAGTT 792  
  
QY 301 GCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTTTATACAAATAGCGCTGTGTTGG 360  
DB |||||||  
793 GCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTTTATACAAAT-AGCGCTGTGTTGG 851  
  
QY 361 GCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAAGTGTACTATCTTGTACCTGCTG 420  
DB |||||||  
852 GCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAAGTGTACTATCTTGTACCTGCTG 911  
  
QY 421 CAGGGCTGCTGGTCAGATGTGGTGAAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 480  
DB |||||||  
912 CAGGGCTGCTGGTCAGATGTGGTGAAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 971  
  
QY 481 GCCACATGATACATCTAAGATTGTAACCTGTAATAAAAAAATGTTCCCTAA 531  
DB |||||||  
972 GCCACATGATACATCTAAGATTGTAACCTGTAATAAAAAAATGTTCCCTAA 1022  
  
RESULT 2  
ABA96630  
ID ABA96630 standard; cDNA; 1040 BP.  
XX  
AC ABA96630;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mouse X-type secretory phospholipase A2 (sPLA2) cDNA.  
XX

Db 733 GCCACCTGCGTTGCTTCTCCTCCATTTCAGAACTCACAACATATAGCCTGTGGAGTT 792

QY 301 GCCAGTCTGATGAAGGTTCAAAGTCCTGGCCTGTTTATACAAATAGCGCTGTGTGG 360

Db 793 GCCAGTCTGATGAAGGTTCAAAGTCCTGGCCTGTTTATACAAAT-AGCGCTGTGTGG 851

QY 361 GCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAAGCTGTACTATCTGTACCTGCTG 420

Db 852 GCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAAGCTGTACTATCTGTACCTGCTG 911

QY 421 CAGGGCTGCTGCTCAGATGTGGGTGAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 480

Db 912 CAGGGCTGCTGCTCAGATGTGGGTGAACACCTGCTTAGGCTTTGCTGTGGTAATAACATT 971

QY 481 GCCACATGATACATCTAAGAATTGTAACCTGTAATAAAAAAATGTTCCCTAA 531

Db 972 GCCACATGATACATCTAAGAATTGTAACCTGTAATAAAAAAATGTTCCCTAA 1022

RESULT 3

AAX79001

ID AAX79001 standard; cDNA; 742 BP.

XX

AC AAX79001;

XX

DT 17-AUG-1999 (first entry)

XX

DE Human phospholipase A2 gene.

XX

KW Human; phospholipase A2; PHPLA2; ovarian tumour; antagonist; antibody;

KW cancer; inflammation; ss.

XX

OS Homo sapiens.

XX

PN WO9924587-A2.

XX

PD 20-MAY-1999.

XX

PP 04-NOV-1998; 98WO-US23555.

XX

PR 07-NOV-1997; 97US-0966317.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Bandman O, Corley NC, Guegler KJ, Hawkins PR, Shah P;

XX

DR WPI; 1999-370674/31.

DR P-PSDB; AAY07481.

XX

PT New human phospholipase A2 protein useful for treating or preventing

PT cancer or inflammation

XX

PS Claim 7; Fig 1; 62pp; English.

XX

CC This sequence represents the coding sequence for a novel 165 amino acid

CC human phospholipase A2 (PHPLA2) protein. The sequence was isolated from

CC clone 816403 from the human tumour cDNA library OVAR101. Antagonists,

CC e.g. antibodies, of PHPLA2 can be used to treat or prevent cancer or

CC inflammation.

XX

SQ Sequence 742 BP; 163 A; 216 C; 189 G; 173 T; 1 other;

Query Match 22.4%; Score 120; DB 20; Length 742;

Best Local Similarity 68.0%; Pred. No. 3.4e-30;

Matches 215; Conservative 0; Mismatches 90; Indels 11; Gaps 3;

QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGTGTGACGAGGCTGGCTTACTGCTG 60

Db 385 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGTGTGACGAGGCTGGCTTACTGCTTA 444

QY 61 GCAGGGACCGAGTACCACTGAAATACCTTCTTCCCTCCATTTTATGTGAGAGGAC 120

Db 445 GCCCAAACCTGAGTACAACTTAAAGTACCTTCTTACCCCAAGTTCCTATGTGAGCGGAC 504

QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174

Db 505 TCGCCCAAGTGTGACTGACTACCTTGACTTGAATGCTCTTTTGCAAGGAAATAAAGC 564

QY 175 TCACTTTCAGTATCACCACAGCATGCAATTGTGCGAGGAGTCAACGGAGGCCAAGT 234

Db 565 GTCTCTCAGTAATGAACAACAGCATTCAGTTATTTGCAGA-AGGGAACCGAAGCCAAGT 623

QY 235 GCTAAAGCCA----CCTGCGTTGCTTTCTCCTTCCATTCCAGGAACCTCACAACATATGAGC 290

Db 624 GATAAAGCCACAACCTTGTGTGCTTTCCCTCCCAATCCCAAGAACTCAGGACTGGAGCC 683

QY 291 CTGTGGAGTTGCCAGT 306

Db 684 CATGTAGGTTTGCAGT 699

RESULT 4

AAS91740

ID AAS91740 standard; cDNA; 1737 BP.

XX

AC AAS91740;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #27544.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PP 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG27553.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity

XX

PS Claim 1; SEQ ID No 27544; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human





XX 24-MAY-2000; 2000JP-0152967.  
XX (SHIO ) SHIONOGI & CO LTD.  
XX Hanaaki K, Imagawa K, Masuta K;  
PI WPI; 2002-097648/13.  
XX P-FSDB; AAM49001.  
PT Antibodies recognizing parts of X-type phospholipase A2 and their use  
PT in immunoassays for diagnosis of cancer and Alzheimer's disease -  
XX Disclosure; Page 40-41; 51pp; Japanese.  
XX The invention relates to antibodies which recognise parts of human X-type  
CC secretory phospholipase A2 (sPLA2; AAM49001, AAM49002). The antibodies of  
CC the invention are specific for the N-terminal propeptide sequence (Glu  
CC -11 to Arg -1) or for the active enzyme (Gly 1 to Asp 123). The invention  
CC also relates to a method of assaying for the X-type sPLA2 propeptide or  
CC active enzyme, and a method for the diagnosis of X-type sPLA2-associated  
CC diseases using the assay. The differing specificities of the antibodies  
CC allows determination of the relative amounts of proenzyme and active  
CC enzyme present. The invention also encompasses drug compositions which  
CC contain antibodies to the sPLA2 active enzyme for the treatment of  
CC X-type sPLA2-associated diseases. The antibodies are used for the  
CC diagnosis and treatment of X-type sPLA2-associated diseases including  
CC cancer of the colon, lung, liver, stomach, kidney, gall bladder, prostate  
CC and pancreas, Alzheimer's disease and liver cirrhosis. The present  
CC sequence is a DNA encoding a 165 residue human X-type sPLA2.  
XX Sequence 1020 BP; 212 A; 304 C; 291 G; 213 T; 0 other;  
SQ  
Query Match 17.8%; Score 95.2; DB 24; Length 1020;  
Best Local Similarity 69.5%; Pred. No. 1.2e-21;  
Matches 146; Conservative 0; Mismatches 58; Indels 6; Gaps 1;  
QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGTGTGACGAGGAGCTGGCTTACTGCGCTG 60  
Db |||||  
801 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGTGTGACGAGGAGTGTCTAACTGCTTA 860  
QY 61 GCAGGGACCGAGTACCACCTGAAATACCTCTTCTCCCTCCATTTATGTGAGAGGAC 120  
Db |||||  
861 GCCCAAACTGAGTACAACTTAAAGTACCTCTTCTACCCCGAGTCTCTATGTGAGCCGGAC 920  
QY 121 TCTCCCAAGTGAATGACAGGC-----TCACATGTCCCTTTGACATGGAAGGCACT 174  
Db |||||  
921 TCGCCCAAGTGTGACTGACTACCTTGACTTGAATGCTCTTTTGACAAAGGAATAAAGC 980  
QY 175 TCACCTTTCAGTGATCACCACCAAGCATGCAA 204  
Db |||||  
981 GTCCTCTCAGTAATGAAAAAATAAATAA 1010  
RESULT 7  
ABL61868/c  
ID ABL61868 standard; DNA; 445 BP.  
XX  
AC ABL61868;  
XX  
DT 15-MAY-2002 (first entry)  
XX  
DE Colon adenocarcinoma related gene sequence SEQ ID NO:205.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200194629-A2.  
XX

PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US10838.  
XX  
PR 05-JUN-2000; 2000US-209473P.  
PR 05-JUN-2000; 2000US-209531P.  
PR 18-SEP-2000; 2000US-233133P.  
PR 18-SEP-2000; 2000US-233617P.  
PR 20-SEP-2000; 2000US-234009P.  
PR 20-SEP-2000; 2000US-234034P.  
PR 20-SEP-2000; 2000US-234052P.  
PR 22-SEP-2000; 2000US-234509P.  
PR 22-SEP-2000; 2000US-234567P.  
PR 25-SEP-2000; 2000US-234923P.  
PR 25-SEP-2000; 2000US-234924P.  
PR 25-SEP-2000; 2000US-235077P.  
PR 25-SEP-2000; 2000US-235082P.  
PR 25-SEP-2000; 2000US-235134P.  
PR 25-SEP-2000; 2000US-235280P.  
PR 26-SEP-2000; 2000US-235637P.  
PR 26-SEP-2000; 2000US-235638P.  
PR 27-SEP-2000; 2000US-235711P.  
PR 27-SEP-2000; 2000US-235720P.  
PR 27-SEP-2000; 2000US-235840P.  
PR 27-SEP-2000; 2000US-235863P.  
PR 28-SEP-2000; 2000US-236028P.  
PR 28-SEP-2000; 2000US-236032P.  
PR 28-SEP-2000; 2000US-236033P.  
PR 28-SEP-2000; 2000US-236034P.  
PR 28-SEP-2000; 2000US-236109P.  
PR 28-SEP-2000; 2000US-236111P.  
PR 29-SEP-2000; 2000US-236842P.  
PR 29-SEP-2000; 2000US-236891P.  
PR 02-OCT-2000; 2000US-237172P.  
PR 02-OCT-2000; 2000US-237173P.  
PR 02-OCT-2000; 2000US-237278P.  
PR 02-OCT-2000; 2000US-237294P.  
PR 02-OCT-2000; 2000US-237295P.  
PR 02-OCT-2000; 2000US-237316P.  
PR 03-OCT-2000; 2000US-237425P.  
PR 03-OCT-2000; 2000US-237598P.  
PR 03-OCT-2000; 2000US-237604P.  
PR 03-OCT-2000; 2000US-237606P.  
PR 03-OCT-2000; 2000US-237608P.  
PR 01-NOV-2000; 2000US-244867P.  
PR 01-NOV-2000; 2000US-245084P.  
XX  
PA (AVAL-) AVALON PHARM.  
XX  
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
DR WPI; 2002-188264/24.  
XX  
PT Screening for anti-neoplastic agent involves exposing cells to a  
PT chemical agent to be tested for anti-neoplastic activity, and  
PT determining a change in expression of a gene of a signature gene set -  
XX  
PS Claim 1; SEQ ID 205; 44pp; English.  
XX  
CC The present invention describes a method (M1) for screening for an  
CC anti-neoplastic agent. The method involves exposing cells to a chemical  
CC agent to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
CC to ABL70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening  
CC an anti-neoplastic agent, and can be used for producing a product which  
CC is the data collected with respect to the anti-neoplastic agent as a  
CC result of M1, and the data is sufficient to convey the chemical  
CC structure and/or properties of the agent. M1 can be used in the  
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,

CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
CC carcinoma, papillary carcinoma and Wilm's tumour.  
XX  
SQ Sequence 445 BP; 99 A; 118 C; 120 G; 106 T; 2 other;  
  
Query Match 17.6%; Score 94; DB 24; Length 445;  
Best Local Similarity 71.4%; Pred. No. 2e-21;  
Matches 140; Conservative 0; Mismatches 50; Indels 6; Gaps 1;  
  
QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60  
Db |||||  
199 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGATTGCTAACTGCTTA 140  
  
QY 61 GCAGGGACCGAGTACCACCTGAAATACCTCTTCCCTCCATTTTATGTGAGAGGAC 120  
Db |||||  
139 GCCCAAACTGAGTACAACTTAAAGTACCTCTTCTACCCCAAGTTCCTATGTGAGCCGGAC 80  
  
QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174  
Db |||||  
79 TCGCCCAAGTGTGACTGACTACCTTGACTTGAAATGCTCTTTTGACAAAGGAATAAAGC 20  
  
QY 175 TCACTTTCAGTGATCA 190  
Db |||||  
19 GTCCTCTCAGTAATGA 4  
  
RESULT 8  
ABL67612/c  
ID ABL67612 standard; DNA; 445 BP.  
XX  
AC ABL67612;  
XX  
DT 15-MAY-2002 (first entry)  
XX  
DE Oesophagus cancer related gene sequence SEQ ID NO:5949.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US10838.  
XX  
PR 05-JUN-2000; 2000US-209473P.  
PR 05-JUN-2000; 2000US-209531P.  
PR 18-SEP-2000; 2000US-233133P.  
PR 18-SEP-2000; 2000US-233617P.  
PR 20-SEP-2000; 2000US-234009P.  
PR 20-SEP-2000; 2000US-234034P.  
PR 20-SEP-2000; 2000US-234052P.  
PR 22-SEP-2000; 2000US-234509P.  
PR 22-SEP-2000; 2000US-234567P.  
PR 25-SEP-2000; 2000US-234923P.  
PR 25-SEP-2000; 2000US-234924P.  
PR 25-SEP-2000; 2000US-235077P.  
PR 25-SEP-2000; 2000US-235082P.  
PR 25-SEP-2000; 2000US-235134P.  
PR 25-SEP-2000; 2000US-235280P.  
PR 26-SEP-2000; 2000US-235637P.  
PR 26-SEP-2000; 2000US-235638P.  
PR 27-SEP-2000; 2000US-235711P.  
PR 27-SEP-2000; 2000US-235720P.  
PR 27-SEP-2000; 2000US-235840P.  
PR 27-SEP-2000; 2000US-235863P.  
PR 28-SEP-2000; 2000US-236028P.

PR 28-SEP-2000; 2000US-236032P.  
PR 28-SEP-2000; 2000US-236033P.  
PR 28-SEP-2000; 2000US-236034P.  
PR 28-SEP-2000; 2000US-236109P.  
PR 28-SEP-2000; 2000US-236111P.  
PR 29-SEP-2000; 2000US-236842P.  
PR 29-SEP-2000; 2000US-236891P.  
PR 02-OCT-2000; 2000US-237172P.  
PR 02-OCT-2000; 2000US-237173P.  
PR 02-OCT-2000; 2000US-237278P.  
PR 02-OCT-2000; 2000US-237294P.  
PR 02-OCT-2000; 2000US-237295P.  
PR 02-OCT-2000; 2000US-237316P.  
PR 03-OCT-2000; 2000US-237425P.  
PR 03-OCT-2000; 2000US-237598P.  
PR 03-OCT-2000; 2000US-237604P.  
PR 03-OCT-2000; 2000US-237606P.  
PR 03-OCT-2000; 2000US-237608P.  
PR 01-NOV-2000; 2000US-244867P.  
PR 01-NOV-2000; 2000US-245084P.  
XX  
PA (AVAL-) AVALON PHARM.  
XX  
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
DR WPI; 2002-188264/24.  
XX  
PT Screening for anti-neoplastic agent involves exposing cells to a  
PT chemical agent to be tested for anti-neoplastic activity, and  
PT determining a change in expression of a gene of a signature gene set -  
XX  
PS Claim 1; SEQ ID 5949; 44pp; English.  
XX  
CC The present invention describes a method (M1) for screening for an  
CC anti-neoplastic agent. The method involves exposing cells to a chemical  
CC agent to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
CC to ABL70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening  
CC an anti-neoplastic agent, and can be used for producing a product which  
CC is the data collected with respect to the anti-neoplastic agent as a  
CC result of M1, and the data is sufficient to convey the chemical  
CC structure and/or properties of the agent. M1 can be used in the  
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
CC carcinoma, papillary carcinoma and Wilm's tumour.  
XX  
SQ Sequence 445 BP; 99 A; 118 C; 120 G; 106 T; 2 other;  
  
Query Match 17.6%; Score 94; DB 24; Length 445;  
Best Local Similarity 71.4%; Pred. No. 2e-21;  
Matches 140; Conservative 0; Mismatches 50; Indels 6; Gaps 1;  
  
QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGCTGGCTTACTGCCTG 60  
Db |||||  
199 GCAGAGAACAAATGCCAAGAACTTTTGTGCAGGTGTGACGAGGAGATTGCTAACTGCTTA 140  
  
QY 61 GCAGGGACCGAGTACCACCTGAAATACCTCTTCTTCCCTCCATTTTATGTGAGAGGAC 120  
Db |||||  
139 GCCCAAACTGAGTACAACTTAAAGTACCTCTTCTACCCCAAGTTCCTATGTGAGCCGGAC 80  
  
QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174  
Db |||||  
79 TCGCCCAAGTGTGACTGACTACCTTGACTTGAAATGCTCTTTTGACAAAGGAATAAAGC 20  
  
QY 175 TCACTTTCAGTGATCA 190  
Db |||||  
19 GTCCTCTCAGTAATGA 4

RESULT 9  
ABL58672  
ID ABL58672 standard; DNA; 465 BP.  
XX  
AC ABL58672;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Human X-type secretory phospholipase A2 encoding sequence.  
XX  
KW Human; X-type secretory phospholipase A2; X-type sPLA2; cancer; colon;  
KW liver; lung; stomach; kidney; gallbladder; prostate; spleen; testis;  
KW ovary; Alzheimer's disease; hepatocirrhosis; immunoassay; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..465  
FT /\*tag= a  
FT /partial  
FT /product= "human X-type secretory phospholipase A2"  
FT /note= "no stop codon present"  
FT 1..96  
FT /\*tag= b  
FT 97..465  
FT /\*tag= c  
XX  
XX  
PN WO200190196-A1.  
XX  
XX  
PD 29-NOV-2001.  
XX  
PP 22-MAY-2001; 2001WO-JP04267.  
XX  
PR 24-MAY-2000; 2000JP-0152967.  
PR 21-NOV-2000; 2000WO-JP08198.  
XX  
PA (SHIO ) SHIONOGI & CO LTD.  
XX  
PI Hanasaki K, Imagawa K, Masuta K;  
XX  
XX WPI; 2002-404351/43.  
DR P-PSDB; ABB80081.  
XX  
XX Immunoassay of X-type phospholipase A2 with antibody recognising part  
PT of it for quantitation of activated version, useful in diagnosis of  
PT e.g. cancer of colon, prostate, ovary or spleen, Alzheimer's disease  
PT and hepatocirrhosis  
XX  
PS Claim 1; Page 50; 59pp; Japanese.  
XX  
CC The invention relates to an antibody that can specifically recognise a  
CC part of X-type secretory phospholipase A2 (X-type sPLA2). The immunoassay  
CC of the invention is used in the diagnosis of e.g. cancer of the colon,  
CC liver, lung, stomach, kidney, gallbladder, prostate, spleen, testis or  
CC ovary, Alzheimer's disease and hepatocirrhosis. The current sequence  
CC represents a human X-type secretory phospholipase A2 encoding sequence.  
XX  
SQ Sequence 465 BP; 90 A; 136 C; 134 G; 105 T; 0 other;  
  
Query Match 16.4%; Score 87.8; DB 24; Length 465;  
Best Local Similarity 79.4%; Pred. No. 2.7e-19;  
Matches 104; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
  
QY 1 GCAGAGAACAAATGCCAAGAACTTTGTGTCAGGTGTGACGAGGAGCTGGCTTACTGCTG 60  
DB |||||  
331 GCAGAGAACAAATGCCAAGAACTTTGTGTCAGGTGTGACGAGGAGATTGCTAACTGCTTA 390  
  
QY 61 GCAGGGACCGAGTACCACCTGAATACCTCTTCTTCCCTCCATTTATGTGAGAGGAC 120  
DB |||||  
391 GCCCAAACTGAGTACAACCTTAAAGTACCTCTTCTACCCCGGAGTCTCTATGTGAGCCGAC 450

QY 121 TCTCCCAAGTG 131  
|||  
Db 451 TCGCCCAAGTG 461  
  
RESULT 10  
ABA96622  
ID ABA96622 standard; DNA; 465 BP.  
XX  
AC ABA96622;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human X-type secretory phospholipase A2 (sPLA2) DNA, SEQ ID NO:3.  
XX  
KW Human; X-type; secretory phospholipase A2; sPLA2; immunoassay;  
KW cancer; tumour; colon; lung; liver; stomach; kidney; gall bladder;  
KW prostate; pancreas; Alzheimer's disease; liver cirrhosis; cytostatic;  
KW nootropic; neuroprotective; hepatotropic; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..465  
FT /\*tag= a  
FT /partial  
FT /product= "Human X-type sPLA2 precursor"  
FT /note= "No stop codon given"  
FT 1..96  
FT /\*tag= b  
FT 97..465  
FT /\*tag= c  
FT /product= "Active human X-type sPLA2"  
XX  
PN WO200190195-A1.  
XX  
XX 29-NOV-2001.  
XX  
PP 21-NOV-2000; 2000WO-JP08198.  
XX  
PR 24-MAY-2000; 2000JP-0152967.  
XX  
PA (SHIO ) SHIONOGI & CO LTD.  
XX  
PI Hanasaki K, Imagawa K, Masuta K;  
XX  
XX WPI; 2002-097648/13.  
DR P-PSDB; AAM49002.  
XX  
XX Antibodies recognizing parts of X-type phospholipase A2 and their use  
PT in immunoassays for diagnosis of cancer and Alzheimer's disease -  
XX  
PS Claim 1; Page 42-43; 51pp; Japanese.  
XX  
CC The invention relates to antibodies which recognise parts of human X-type  
CC secretory phospholipase A2 (sPLA2; AAM49001, AAM49002). The antibodies of  
CC the invention are specific for the N-terminal propeptide sequence (Glu  
CC -11 to Arg -1) or for the active enzyme (Gly 1 to Asp 123). The invention  
CC also relates to a method of assaying for the X-type sPLA2 propeptide or  
CC active enzyme, and a method for the diagnosis of X-type sPLA2-associated  
CC diseases using the assay. The differing specificities of the antibodies  
CC allows determination of the relative amounts of proenzyme and active  
CC enzyme present. The invention also encompasses drug compositions which  
CC contain antibodies to the sPLA2 active enzyme for the treatment of  
CC X-type sPLA2-associated diseases. The antibodies are used for the  
CC diagnosis and treatment of X-type sPLA2-associated diseases including  
CC cancer of the colon, lung, liver, stomach, kidney, gall bladder, prostate  
CC and pancreas, Alzheimer's disease and liver cirrhosis. The present  
CC sequence is a DNA encoding a 155 residue human X-type sPLA2.  
XX  
SQ Sequence 465 BP; 90 A; 136 C; 134 G; 105 T; 0 other;  
  
Query Match 16.4%; Score 87.8; DB 24; Length 465;



Best Local Similarity 79.4%; Pred. No. 2.7e-19;  
Matches 104; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
Qy 1 GCAGAGAACAAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGCTGGCTTACTGCTG 60  
Db 331 GCAGAGAACAAATGCCAAGAACTTTTGTGAGGTGTGACGAGGAGATTGCTAACTGCTTA 390  
Qy 61 GCAGGACCGAGTACCACCTGAATACCTCTTCTTCCCTCCATTTATGTGAGAAAGGAC 120  
Db 391 GCCCAACTGAGTACAACCTTAAAGTACCTCTTCTACCCCGAGTTCCTATGTGAGCCGGAC 450  
Qy 121 TCTCCCAAGTG 131  
Db 451 TCGCCCAAGTG 461

RESULT 11  
ABN57123  
ID ABN57123 standard; DNA; 65 BP.  
XX  
AC ABN57123;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:29871.  
XX  
KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
OS Mus musculus.  
XX  
PN WO200210449-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 20-JUL-2001; 2001WO-IB01903.  
XX  
PR 28-JUL-2000; 2000US-221607P.  
PR 02-MAY-2001; 2001US-287724P.  
XX  
PA (COMP-) COMPUGEN INC.  
XX  
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX  
DR WPI; 2002-257383/30.  
XX

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes  
Example 1; SEQ ID 29871; 47pp; English.  
The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in

CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 65 BP; 12 A; 13 C; 22 G; 18 T; 0 other;  
Query Match 11.9%; Score 63.4; DB 24; Length 65;  
Best Local Similarity 98.5%; Pred. No. 2e-11;  
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 412 TACCTGCTGCAGGGCTGCTGTCAGATGTTGGTGAACACCTGCTTAGGCTTGGTGGT 471  
Db 1 TACCTGCTGTCAGGGCTGCTGTCAGATGTTGGTGAACACCTGCTTAGGCTTGGTGGT 60  
Qy 472 AATAA 476  
Db 61 AATAA 65  
RESULT 12  
AAS67219/c  
ID AAS67219 standard; cDNA; 758 BP.  
XX  
AC AAS67219;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #3023.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR P-PSDB; ABG03032.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX  
PS Claim 1; SEQ ID No 3023; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity



CC (b) is the IGF (insulin-like growth factor)-1 promoter. (2) vectors  
CC containing (A); and (3) host cells containing the vector of (2). (A) are  
CC used in gene therapy of a wide range of cancers, particularly carcinoma  
CC (of bladder, liver, ovary, cervix, lung, breast, oesophagus, thyroid, or  
CC squamous cell carcinoma of head and neck); hepatoblastoma;  
CC rhabdomyosarcoma; astrocytoma; ganglioblastoma and neuroblastoma. The  
CC specified regulators provide tumour-specific expression. The present  
CC sequence represents a specifically claimed human H19 promoter sequence  
CC from the present invention.

XX  
SQ Sequence 830 BP; 151 A; 245 C; 312 G; 122 T; 0 other;

Query Match 6.6%; Score 35.4; DB 20; Length 830;  
Best Local Similarity 55.2%; Pred. No. 0.3;  
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 70 GAGTACCACCTGAAATACCTCTTCTTCCCTCCATTTTATGTGAGAAGGACTCTCCCAAG 129  
Db 796 GTGGCCCGCCAGAAATTCGCGCCCTGCGCGGCAATCAGAGCAGGGCCCTCCCGAG 737  
Qy 130 TGCAATTGACAGGCTCACATGTCCCTTTCACATGGAAACGCACTTTCAGTGATC 189  
Db 736 GGCCCCCGCAGGGCCACCTCCGCGCTGGACAGTTCAGACACGCTCTCTCACCAGC 677

Qy 190 ACCAA 194  
Db 676 ACCCA 672

RESULT 15  
AAA72969/c  
ID AAA72969 standard; DNA; 830 BP.  
XX  
AC AAA72969;  
XX  
DT 23-NOV-2000 (first entry)  
XX Human H19 promoter nucleotide sequence SEQ ID NO:1.  
XX Human; H19 promoter; H19 enhancer; expression; cytotoxic; tumour;  
KW transcription; regulation; cancer; cytostatic; gene therapy; ds.  
XX Homo sapiens.  
XX US6087164-A.  
XX 11-JUL-2000.  
XX  
PF 01-OCT-1998; 98US-0165240.  
XX  
PR 03-OCT-1997; 97US-0943608.  
XX  
PA (YISS ) YISSUM RES & DEV CO.  
XX Ayesha S, Hochberg A;  
XX WPI; 2000-531346/48.  
XX  
PT Expression of heterologous sequences especially genes encoding  
PT cytotoxic products in tumor cells for treating cancer, by transforming  
PT tumor cells with heterologous sequence linked with a regulatory  
PT sequence -  
XX  
PS Claim 4; Fig 1A-C; 33pp; English.

CC The present invention describes a method for expressing a heterologous  
CC sequence in a tumour cell. The method comprises introducing into the  
CC tumour cell a polynucleotide (I) comprising a regulatory sequence  
CC operably linked to a heterologous sequence encoding a cytotoxic gene  
CC product, where the regulatory sequence is derived from a genomically  
CC imprinted gene that is specifically expressed in the tumour cell. The  
CC present sequence represents a specifically claimed human H19 promoter  
CC nucleotide sequence use in the method of the invention. The method is

CC useful for selective expression of heterologous genes in tumour cells  
CC in a subject having bladder, hepatocellular, ovarian, cervical, lung  
CC or breast carcinoma, squamous cell carcinoma in head and neck,  
CC oesophageal and thyroid carcinoma, astrocytoma, ganglioblastoma,  
CC neuroblastoma, hepatoblastoma or rhabdomyosarcoma. This method is useful  
CC for treating wide variety of cancers and hyperproliferative conditions.  
CC The method can be used in gene therapy techniques.

XX Sequence 830 BP; 151 A; 245 C; 312 G; 122 T; 0 other;

Query Match 6.6%; Score 35.4; DB 21; Length 830;  
Best Local Similarity 55.2%; Pred. No. 0.3;  
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 70 GAGTACCACCTGAAATACCTCTTCTTCCCTCCATTTTATGTGAGAAGGACTCTCCCAAG 129  
Db 796 GTGGCCCGCCAGAAATTCGCGCCCTGCGCGGCAATCAGAGCAGGGCCCTCCCGAG 737  
Qy 130 TGCAATTGACAGGCTCACATGTCCCTTTCACATGGAAACGCACTTTCAGTGATC 189  
Db 736 GGCCCCCGCAGGGCCACCTCCGCGCTGGACAGTTCAGACACGCTCTCTCACCAGC 677  
Qy 190 ACCAA 194  
Db 676 ACCCA 672

Search completed: December 19, 2003, 13:30:33  
Job time : 260 secs



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OM nucleic - nucleic search, using sw model

Run on: December 19, 2003, 12:39:44 ; Search time 2067 Seconds  
(without alignments)  
6290.709 Million cell updates/sec

Title: US-09-620-607B-34  
Perfect score: 535  
Sequence: 1 gcagagaacaatgccga.....aaaaaatgttcctaactgg 535

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5:	em_estov:*	5:	em_estov:*
6:	em_estpl:*	6:	em_estpl:*
7:	em_estro:*	7:	em_estro:*
8:	em_hic:*	8:	em_hic:*
9:	gb_est1:*	9:	gb_est1:*
10:	gb_est2:*	10:	gb_est2:*
11:	gb_hic:*	11:	gb_hic:*
12:	gb_est3:*	12:	gb_est3:*
13:	gb_est4:*	13:	gb_est4:*
14:	gb_est5:*	14:	gb_est5:*
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28:	gb_ges1:*	28:	gb_ges1:*
29:	gb_ges2:*	29:	gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520.4	97.3	611	10	BB015940
2	520.4	97.3	823	11	AK076921
3	458.4	85.7	486	4	BX528749
4	453.6	84.8	480	9	AA611431

5	382.8	71.6	408	9	AA607557	AA607557 vo44d05.r
6	371.6	69.5	834	12	BG964576	BG964576 602832255
7	297	55.5	587	10	BB615766	BB615766 BB615766
8	284.4	53.2	322	10	BB548845	BB548845 BB548845
9	284	53.1	311	9	AV053175	AV053175 AV053175
10	270.6	50.6	314	9	AV075661	AV075661 AV075661
11	266.4	49.8	288	9	AV081069	AV081069 AV081069
12	260.8	48.7	497	9	AA851843	AA851843 EST194611
13	242.6	45.3	701	10	BF584442	BF584442 602098336
14	239.4	44.7	325	10	BB552490	BB552490 BB552490
15	233.6	43.7	260	9	AV215819	AV215819 AV215819
16	213.8	40.0	245	10	BB535230	BB535230 BB535230
17	199.2	37.2	225	9	AV079620	AV079620 AV079620
18	196.6	36.7	239	9	AV370437	AV370437 AV370437
19	196.2	36.7	238	9	AV370433	AV370433 AV370433
20	165	30.8	382	12	BM386094	BM386094 UI-R-DN1-
21	162.2	30.3	201	9	AV073732	AV073732 AV073732
22	129.4	24.2	245	9	AA512293	AA512293 vj19h01.r
23	94	17.6	445	14	N93958	N93958 zb74f04.e1
24	93.6	17.5	543	9	AW292929	AW292929 UI-H-BW0-
25	91.2	17.0	213	10	BF001580	BF001580 790C06.x
26	86.4	16.1	571	10	BF189854	BF189854 235602 MA
27	85.4	16.0	505	10	BF189855	BF189855 235603 MA
28	79.8	14.9	653	14	CB456511	CB456511 713776 MA
29	79.6	14.9	461	10	BE755026	BE755026 208730 MA
30	78.8	14.7	495	10	BF077514	BF077514 227437 MA
31	78.6	14.7	652	14	CB454932	CB454932 711760 MA
32	61.2	11.4	558	12	BM087924	BM087924 501240 MA
33	49.2	9.2	618	12	BM739473	BM739473 K-EST0009
34	45	8.4	445	12	BM055133	BM055133 ie94h05.x
35	44.6	8.3	179	12	BM030728	BM030728 495216 MA
36	44.6	8.3	735	13	BU343843	BU343843 603525637
37	39.6	7.4	616	13	BU397712	BU397712 603536856
38	39.6	7.4	642	13	BU419716	BU419716 603954957
39	39.6	7.4	653	13	BU124546	BU124546 603147566
40	39.6	7.4	722	13	BU346925	BU346925 603523604
41	38.6	7.2	1018	29	CNS05478	AL320381 Tetraodon
42	38.2	7.1	284	9	AI165840	AI165840 A092P61U
43	38	7.1	609	13	BU837617	BU837617 T103G12 P
44	38	7.1	660	12	BI400547	BI400547 MI-P-AY1-
45	38	7.1	849	10	BF678392	BF678392 602085823

ALIGNMENTS

RESULT 1  
BB015940  
LOCUS BB015940 RIKEN full-length enriched, adult male testis (DH10B) Mus  
DEFINITION musculus cDNA clone 4930556P12 3' similar to AF166097 Mus musculus  
group X secreted phospholipase A2 (Pla2g10), mRNA sequence.  
ACCESSION BB015940  
VERSION BB015940.2 GI:16257430  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda  
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,  
Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sakai,K., Sano,H., Sasaki  
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,  
Tagami,M., Tagawa,A., Takahashi,P., Takeda,Y., Tanaka,T., Toya,T.,  
Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

TITLE Unpublished  
JOURNAL On Jun 2, 2000 this sequence version replaced gi:8186926.  
COMMENT Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute



MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

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11076861  
4  
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 823)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE  
JOURNAL

Direct Submission  
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

FEATURES  
source

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Matches 532; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
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ID BX528749 standard; RNA; EST; 486 BP.

XX BX528749;

XX BX528749.1

SV 27-MAY-2003 (Rel. 75, Created)

DT 27-MAY-2003 (Rel. 75, Last updated, Version 1)

XX

DE RZPD Mus musculus cDNA clone IMAGE998L172633 = IMAGE:1053472 5' EST.

XX EST; expressed sequence tag.

KW



XX Mus musculus (house mouse)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
XX [1]  
RN 1-486  
RA Heil O., Ebert L., Neubert P., Peters M., Radelof U., Schneider D.,  
RA Korn B.;  
RT Submitted (28-MAY-2003) to the EMBL/GenBank/DBJ databases.  
RL RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer  
RL Feld 580, D-69120 Heidelberg, Germany  
XX RZPD; IMAGp998L172633.  
CC RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
CC Mouse Unigeneset - RZPD2 (RZPDLIB NO.981)  
CC http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981  
CC Contact: Ina Rofls  
CC RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
CC Heubnerweg 6, D-14059 Berlin, Germany  
CC Tel: +49 30 32639 101  
CC Fax: +49 30 32639 111  
CC www.rzpd.de  
CC This clone is available royalty-free from RZPD;  
CC contact RZPD (clone@rzpd.de) for further information.  
CC Seq primer: T7, Primer sequence: TAATACGACTCACTATAGG  
XX Key Location/Qualifiers  
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FT strand cDNA was primed with a Not I - oligo(dT) primer  
FT [5'TGTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTT  
FT TTTTTTTTTTTT 3']; double-stranded cDNA was ligated to  
FT Eco RI adaptors [AATTCGTCACATG], digested with NotI and  
FT cloned into the NotI and EcoRI sites of the pT7T3D-Paci  
FT vector. Library constructed by R. Barstead (Oklahoma  
FT Medical Research Foundation)."  
FT /note="polyA-like signal AATAAA at -24 of polyA tail"  
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181 ACCTGCGTTTGTCTCTCTCCATTCCAGGAACCTACAACTATGAGCCTGTGGAGTTGCC 240  
304 AGTCTGATGAAGGTTCAAAGTCTGGGCGCTGTTTTATACAAATAAGCGCTGTGGGCG 363  
241 AGTCTGATGAAGGTTCAAAGTCTGGGCGCTGTTTTATACAAAT-AGCGCTGTGGGCG 299

QY 364 TGGTATACTTTTGAATTCAGCCTTTATGAGAAGCTGTACTATCTTGTACCTGCTGCAG 423  
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DEFINITION vo5l909.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA  
clone IMAGE:1053472 5', mRNA sequence.  
ACCESSION AA611431  
VERSION AA611431.1 GI:2461510  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 480)  
REFERENCE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
AUTHORS Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:585048  
Putative full length read  
vector to vector length is  
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/lab\_host="DH10B"  
/clone\_lib="Barstead mouse irradiated colon MPLRB7"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
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from 8 week old mouse. Colon was harvested 72 hours after  
irradiation with 1400 Gys. 1st strand cDNA was primed  
with a Not I - oligo(dT) primer  
[5'TGTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors [AATTCGATCCTTG], digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. Library constructed by Bob Barstead."  
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Best Local Similarity 98.9%; Pred. No. 2e-131;  
Matches 467; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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LOCUS
DEFINITION
AA607557.1 GI:2454992
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 408)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:584321
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1. 408
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from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
[5'TGTTACGAATCTGAAGTGGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors [AATTCGGATCCTG], digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library constructed by Bob Barstead."
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Best Local Similarity	99.0%	Pred. No. 3.7e-109;		
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DEFINITION
BG964576
EST.
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ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 834)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Db 351 GCAGGACCGAGTACCACCTGAAATACCTCTTCTTCCCTCCATTTTATGTGAGAGGAC 410

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Qy 181 TCAGTGTATCACCACAGCATGCAATTTGTGAGGAGAGTCAACGGAGCCCAAGTGCTAAA 240

Db 471 TCAGTGTATCACCACAGCATGCAATTTGTGAGGAGAGTCAACGGAGCCCAAGTGCTAAA 530

Qy 241 GCCACCTGCGTTGCTTTCTCTTCCATTGAGGAACTCACAACATGAGCCTGTGGA 297

Db 531 GCCACCTGCGTTGCTTTCTCTTCCATTGAGGAACTCACAACATGAGCCTGTGGA 587

RESULT 8

BB548845

LOCUS

DEFINITION

BB548845 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230012J10 3' similar to AF166097

Mus musculus group X secreted phospholipase A2 (Pla2g10) mRNA, mRNA sequence.

BB548845

BB548845.1 GI:9620273

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 322)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,K., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Teunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1. .322

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="E230012J10"

/sex="female"

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/dev\_stage="2 days pregnant adult"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, 2 days pregnant adult female oviduct"

/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5,

GAGAGAGAGCGCGCAACTCGAGTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5,

GAGAGAGAGATTCTCGAGTTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 82 a 68 c 77 g 95 t

ORIGIN

Query Match 53.2%; Score 284.4; DB 10; Length 322;

Best Local Similarity 94.7%; Pred. No. 3.3e-78;

Matches 305; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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Db 1 GGAGAATTACCGAGCGCAAGTGCTAAAGCCACCTGCGTTTGTCTTCTCTCCATTCAG 60

QY 273 GAACTCACAACATATGAGCTGTGGAGTTGCCAGTCTGATGAAGGTTCAAAGTCTCTGGGCC 332

Db 61 GAACTCAAAACTATGAGCTGTGGAGTTGCCAGTCTGATGAAGGTTCAAAGTCTCTGGGCC 120

QY 333 TGTTTTATACAAATAAGCGCTGTGTGGCGGTGGTATACTTTTGAATTCAGCCTTTAT 392

Db 121 TGTTTTATACAAA-AAGCGCTGTGTTCGGCGTGGTATACTTTTGAATTCAGCCTTTAT 179

QY 393 GAGAAAGCTGTACTATCTTGTACTCTGTGCAGGGCTGCTGGTGCAGATGTGGTGAACACCT 452

Db 180 GAGAAAGCTGTACTCTTGTACTCTGTGCAGGGCTGCTGGTGTAGATGTGGTGAACACCT 239

QY 453 GCTTAGGCTTTGTGTGTAATAACATTGCCACATGATACATCTAAGAAATTGTAACCTGA 512

Db 240 GCTTAGGCTTGGCTGTGGTAATAACATTGCCGCATGATAAATCTAAGAATTGTAACCTGA 299

QY 513 ATAAAAAAATGTTCCCTAACTG 534

Db 300 ATAAAAAAATGTTCCCAACTG 321

RESULT 9

AV053175

LOCUS

DEFINITION

AV053175 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA clone 1810025L01, mRNA sequence.

ACCESSION

AV053175

VERSION

AV053175.1 GI:5152922

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 311)

Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Naitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,



Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,  
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
RIKEN Mouse ESTs  
Unpublished  
Contact: Chie Owa  
Genome Science Laboratory  
RIKEN  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-9145  
Fax: 81-298-36-9098  
Email: genome-res@rtc.riken.go.jp  
Thermotabilization and thermoactivation of thermolabile enzymes by  
trehalose and its application for the synthesis of full length cDNA  
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
Please visit our web site (http://genome.rtc.riken.go.jp) for  
further details.

FEATURES  
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QY 283 CTATGAGCCTGTGGAGTTGCCAGTCTGATGAAGTTCAAAGTCTCTGGCCTGTTTATAC 342  
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QY 343 AAATAAGCGCTGTGTGGCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAAGCTGT 402  
Db 121 AAAT-AGCGCTGTGTGGCGTGGTTACTTTTGAATTCAGCCTTTATGAGAAGCTGT 179  
QY 403 ACTATCTTGACCTGCTGCAGGCTGCTGTCAGATGTGGTGAACACCTGCTTAGGCTT 462  
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QY 463 TGCTGTGGTAATAACATTGCCACATGATACATCTAAGAATTGTAATAAAAAAAT 522  
Db 240 GGCTGTGGTAATAACATTGCCACATGATACATCTAAGAATTGTAATAAAAAAAT 299  
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Db 300 GTTCCCTAACTG 311

RESULT 10  
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LOCUS  
DEFINITION AV075661 Mus musculus stomach C57BL/6J adult Mus musculus cDNA  
clone 2210014N10, mRNA sequence.  
ACCESSION AV075661  
VERSION AV075661.1 GI:5195489  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 314)  
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,  
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara  
A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,  
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,  
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara  
Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,  
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,  
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
RIKEN Mouse ESTs  
Unpublished  
Contact: Chie Owa  
Genome Science Laboratory  
RIKEN  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-9145  
Fax: 81-298-36-9098  
Email: genome-res@rtc.riken.go.jp  
Thermotabilization and thermoactivation of thermolabile enzymes by  
trehalose and its application for the synthesis of full length cDNA  
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
Please visit our web site (http://genome.rtc.riken.go.jp) for  
further details.

TITLE  
JOURNAL  
COMMENT

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LOCUS  
DEFINITION AV081069 Mus musculus stomach C57BL/6J adult Mus musculus cDNA  
clone 2210417E11, mRNA sequence.

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VERSION AV081069.1 GI:5212517
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 288)
AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomimaga,N.,
Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs
JOURNAL Unpublished
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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Db 61 TGATGAAGGTTCAAAGTCCTGGGCTGTTTATACAAAT-AGCGCTGTGTGGCGTGGT 119
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AA851843/c

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DEFINITION EST194611 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
RSPAN43 3' end, mRNA sequence.
ACCESSION AA851843
VERSION AA851843.1 GI:2939383
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 497)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat
Gene Index
JOURNAL Unpublished
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
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QY 26 TGTGCAGGTGTGACGAGGAGCTGGCTTACTGCTGGCAGGACCGAGTACCACCTGAAT 85
Db 497 TATGCAGGTGTGATGAGACGCTCGCATACTGCCTGGCAGACACAGAGTACCACCTG-AAT 439
QY 86 ACCTCTTCTCCCTCCATTATGTGAGAAGGACTCTCCCAAGTCAATTGACAGGCTC 145
Db 438 ACCTCTTCTCCCTTCGGTTTATGTGAGAAGGACTCACCCAAGTCAACTAATAGGCTG 379
QY 146 ACATGTCCCTTTGCACATGGAACGCACCTTCATCTTCAGTGATCACCAACAGCATGCAAT 205
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QY 266 CATTGAGGAACCTCAAACTATGAGCCTGTGGAGTTGCCAGTCTGATGAAGTTCAAAGTC 325
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QY 386 CCTTTATGAGAAGCTGTACTATCTTGTACCTGCTGC--AGGGCTGCTGGTCAGATGTGG 443
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	35.4	6.6	830	4	US-09-568-059-1
C 5	35.2	6.6	1830121	4	US-09-557-884-1
C 6	35.2	6.6	1830121	4	US-09-643-990A-1
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10	33	6.2	993	4	US-09-328-352-2045
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C 13	29.8	5.6	53332	4	US-09-801-861-3
C 14	29.6	5.5	569	1	US-08-318-905-19
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23	29.2	5.5	771	4	US-09-252-991A-9099
C 24	29.2	5.5	810	4	US-09-252-991A-8770
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27	29.2	5.5	3815	4	US-08-936-165A-196

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C 29	29	5.4	2803	3	US-08-949-588-1	Sequence 1, Appli
C 30	28.8	5.4	298	4	US-09-313-294A-6113	Sequence 6113, Ap
31	28.8	5.4	2549	1	US-08-470-720-2	Sequence 2, Appli
32	28.8	5.4	3989	1	US-08-327-494A-1	Sequence 1, Appli
33	28.8	5.4	3989	1	US-08-327-494A-3	Sequence 3, Appli
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C 38	28.6	5.3	1975	4	US-09-328-571A-12	Sequence 12, Appl
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C 43	28.4	5.3	2201	4	US-09-149-476-245	Sequence 245, App
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C 45	28.4	5.3	4655	4	US-09-207-914-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-08-966-317-2  
; Sequence 2, Application US/08966317  
; Patent No. 6103469  
; GENERAL INFORMATION:  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/966,317  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0403 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 742 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: OVARTUT01  
; CLONE: 816403  
US-08-966-317-2

Query Match 22.4%; Score 120; DB 3; Length 742;  
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Patent No. 6306833  
GENERAL INFORMATION:  
APPLICANT: Hochberg, Abraham  
APPLICANT: Ayesha, Suhail  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING  
TUMOR-SPECIFIC CYTOTOXICITY  
FILE REFERENCE: 9457-0014-999  
CURRENT APPLICATION NUMBER: US/09/568,059  
PRIOR FILING DATE: 2000-05-10  
PRIOR APPLICATION NUMBER: 09/165,240  
PRIOR FILING DATE: 1998-10-01  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
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US-09-568-059-1

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Best Local Similarity 55.2%; Pred. No. 0.053;  
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
QY 70 GAGTACCACCTGAAATACCTCTTCTTCCCTCCATTTATGTGAGAGGACTCTCCCAAG 129  
Db 796 GTGGCCCGCCAGAAATTCGGCCCTGCGCTGCGGCCAATCAGAGCGGGCCCTCCCGAG 737  
QY 130 TGCAATTGACAGGCTCACATGTCCCTTTGCACATGGAACGCACTTCATTTCACTGATC 189  
Db 736\*GGCCCCCGCAGGGCCCACTCCGCCCTGGACAGTCCAGCACACGTCTCTCTCACCAGC 677  
QY 190 ACCAA 194  
Db 676 ACCCA 672

RESULT 5  
US-09-557-884-1/c  
Sequence 1, Application US/09557884  
Patent No. 6506581  
GENERAL INFORMATION:  
APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557,884  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: JUN-5-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB186P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1  
Query Match 6.6%; Score 35.2; DB 4; Length 1830121;  
Best Local Similarity 49.5%; Pred. No. 4.7;  
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;  
QY 201 GCAATTTGTGAGGAGAGTCAACCGGAGGCAAGTGCTAAAGCCACCTGCGTTTCTTCT 260  
Db 1392777 GAAGTTTATCCATGCAAGAACGGCTTGCCTTCATCTAATGATTTCTGAATATATTTT 1392718  
QY 261 CCTTCCATTGAGGAACCTCAACACTATGAGCCTGTGGAGTTGCCAGTCTGATGAAGTTCA 320  
Db 1392717 CGCTTCATCAATGATGAATAAGGGATGGTTTGATCTTTTGGCCTGAGAGTAAACCGCA 1392658  
QY 321 AGTCTCTGGCCTGTTTATACAAATAAGCGCTGTGTGGCGGTGATGATCTTTTGA 380  
Db 1392657 AAGTCTCTGACCGGTAATGCGGATATCTCCAAAGTAGCGCGCTTACTTCTGGAT 1392598  
QY 381 TTCA 384  
Db 1392597 TTCA 1392594

RESULT 6  
US-09-643-990A-1/c  
Sequence 1, Application US/09643990A  
Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter  
TITLE OF INVENTION: The Nucleotide sequence of  
the Haemophilus influenzae Rd Genome, Fragments  
Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:



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;
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match
Best Local Similarity 6.6%; Score 35.2; DB 4; Length 1830121;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 201 GCAATTTGTGCGAGAGTACCGGAGGCCCAAGTCTAAAGCCACCTGCGTTTGTCTTCT 260
Db 1392777 GAAGTTTATCCATGCAAGAACGGCTTGCCCTTCATCTAATGATTCCTTGAATATATTTT 1392718

QY 261 CCTTCCATTGAGGAATCAAACTATAGAGCCCTGTGGAGTTGCCAGTCTGATGAAGTTCA 320
Db 1392717 CGCTTCATCAATGAAATAAGGGATGGTTTGATCTTTTGGCCTGAGAGTAACCGCA 1392658

QY 321 AAGTCTGGGCTGTGTTTATACAAATAAGCGCTGTGTGGCGTGGTATACTTTTGA 380
Db 1392657 AAGTTCTTGTAACCGTAAATGCGGATTAATCTCCAAAGTAGGCGGCTTACTTCTGGGAT 1392598

QY 381 TTCA 384
Db 1392597 TTCA 1392594
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RESULT 7
US-09-165-240-2/c
; Sequence 2, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
; APPLICANT: Hochberg, Abraham
; APPLICANT: Ayes, Suhail
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
; FILE REFERENCE: 9457-0014-999
; CURRENT APPLICATION NUMBER: US/09/165,240A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: US 08/943,608
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-165-240-2
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Query Match
Best Local Similarity 6.3%; Score 33.8; DB 3; Length 833;
Matches 65; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 78 CCTGAAATACCTCTTCTTCCCTCCATTTTATGTGAGAGGACTCTCCCAAGTGCAATTG 137
Db 775 CCAGAATTCCTGCGCCCTGCGCCCAATCAGAGCAGGCGCCCTCCCGAGGGCCCCCG 716

QY 138 ACAGGCTCACATGTCCCTTTCACATGGAACGCATTCCTTTCAGTGATCACC 194
Db 715 CAGGGCCCACTCCGCGCTGGACAGTTCAGACACACGTCTCTCTCACCAGCACCA 659
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RESULT 8
US-09-568-059-2/c
; Sequence 2, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
; APPLICANT: Hochberg, Abraham
; APPLICANT: Ayes, Suhail
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
; FILE REFERENCE: 9457-0014-999
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; CURRENT APPLICATION NUMBER: US/09/568,059
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/165,240
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-568-059-2

Query Match
Best Local Similarity 6.3%; Score 33.8; DB 4; Length 833;
Matches 65; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 78 CCTGAAATACCTCTTCTTCCCTCCATTTTATGTGAGAGGACTCTCCCAAGTGCAATTG 137
Db 775 CCAGAATTCCTGCGCCCTGCGCCCAATCAGAGCAGGCGCCCTCCCGAGGGCCCCCG 716

QY 138 ACAGGCTCACATGTCCCTTTCACATGGAACGCATTCCTTTCAGTGATCACC 194
Db 715 CAGGGCCCACTCCGCGCTGGACAGTTCAGACACACGTCTCTCTCACCAGCACCA 659
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RESULT 9
US-08-894-324A-1/c
; Sequence 1, Application US/08894324A
; Patent No. 6204437
; GENERAL INFORMATION:
; APPLICANT: Grierson, Donald
; APPLICANT: Blume, Beatrice
; APPLICANT: Hamilton, Andrew
; APPLICANT: Holdsworth, Michael
; APPLICANT: Barry, Cornelius
; TITLE OF INVENTION: DNA Constructs and Plants Incorporating
; TITLE OF INVENTION: Them
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca Inc.
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,324A
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00564
; FILING DATE: 11-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95056081.1
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33712
; REFERENCE/DOCKET NUMBER: SEE 45003/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; ORIGINAL SOURCE:
; ORGANISM: ACO1 PROMOTER
US-08-894-324A-1

Query Match      6.2%; Score 33.4; DB 3; Length 1925;
Best Local Similarity 57.0%; Pred. No. 0.4;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 419 TGCAGGGCTGCTGTCAGATGTGGTGAACACCTGCTTAGGCTTTGCTGTGTAATAACA 478
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Db 1856 TGAAGAGATGAATATCAATGTTTGATGTACAAATAATGAGGCTTTGAAAGGGTATTATA 1797

QY 479 TTGCCACATGATACATCTAAGAATTGTAACGTGTAATAAAAAAATGTT 525
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Db 1796 GTAGAAGATATTAAAGTAGAGAATTATAATTTAAATGAATAATTATT 1750

RESULT 10
US-09-328-352-2045
; Sequence 2045, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2045
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2045

Query Match      6.2%; Score 33; DB 4; Length 993;
Best Local Similarity 45.5%; Pred. No. 0.38;
Matches 117; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 230 CAAGTGCTAAAGCCACCTGCGTTTGCTTTCTCTTCCATTTCAGGAACCTCACAACCTATGAG 289
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Db 664 CCAGTTGACAAACTATTTGAACTATTGATTTTACGAGTCAGAAAGCTAACCGTTTAATG 723

QY 290 CCTGTGGAGTTGCCAGTCTGATGAAGGTTCAAAGTCTGGCCCTGTTTATACAAATAAG 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 GAAGCTAAACTTCCACTTCCAGCTTATGAGCAAGTCGTTAAAGCGTCTCATACCTTTAAC 783

QY 350 CGCTGTGTTGGCGTGGTATACCTTTTGAATTCAGCCTTTATGAGAGCTGTACTATCT 409
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QY 410 TGTACCTGCTGCAGGGCTGCTGGTCAGATGCGGTGAACACCTGCTTAGGCTTTGCTGTG 469
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Db 844 CGTACTTTGGCGCGCGCTATTGTCACAAAGTTATGTACAAGCAGCTGCAGAGCTTGGCTTC 903

QY 470 GTAATAACATTGCCACA 486
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Db 904 CCAATGGCAGAACCA 920

RESULT 11
US-08-545-528D-1/c
; Sequence 1, Application US/08545528D
; Patent No. 6537773
; GENERAL INFORMATION:
; APPLICANT: Fraser et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
; Patent No. 6537773
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PBI93P1
; CURRENT APPLICATION NUMBER: US/08/545,528D
; CURRENT FILING DATE: 1995-10-19
; PRIOR APPLICATION NUMBER: US 08/488,018

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; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/473,545
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 580073
; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

Query Match      6.0%; Score 32.2; DB 4; Length 580073;
Best Local Similarity 56.0%; Pred. No. 26;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 275 ACTCACAACTATGAGCCTGTGGAGTTGCCAGTCTGATGAAGTTCAAAGTCTTGGGCTG 334
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Db 476223 ACTTAGAAAAATTACAACGTTGGCTTTGACATTCTATTATGTTGAGGCACTGATCATG 476164

QY 335 TTTTATACAAATAAGCGCTGTGTGGCGTGGTATACCTTTTGAATTC 383
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Db 476163 AAGGACATATTAAAGGATGTATTGTGCACTTTGATGCTTTTAAAAAATAC 476115

RESULT 12
US-09-620-312D-641/c
; Sequence 641, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 641
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (265)..(1422)
US-09-620-312D-641

Query Match      5.8%; Score 30.8; DB 4; Length 2052;
Best Local Similarity 51.4%; Pred. No. 3.2;
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 126 CAAGTGCAATTGACAGGCTCACATGTCCCTTTGACATGGAAACGCACTTCACTTTCAGT 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1923 CAAGCCCCAGTCCCCACCTGGGAAGGCGCTGGTGCATGGGAGGCGAGGTGAGGTCCT 1864

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

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SUMMARIES

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1	120	22.4	742	14	US-10-124-591-2
2	94	17.6	445	10	US-09-962-832-63
3	94	17.6	445	13	US-09-873-367C-205
4	63.4	11.9	65	13	US-09-908-975-29871
5	37.4	7.0	815	13	US-10-027-632-155029
6	37.4	7.0	815	14	US-10-027-632-155029
7	35.4	6.6	3489	13	US-09-873-367C-444
8	35.4	6.6	3497	15	US-10-208-408-36
9	35.2	6.6	1830121	15	US-10-329-960-1
10	34.6	6.5	630	13	US-10-027-632-290510
11	34.6	6.5	630	14	US-10-027-632-290510
12	34.2	6.4	630	13	US-10-027-632-290511
13	34.2	6.4	630	14	US-10-027-632-290511
14	33.6	6.3	1204	9	US-09-822-849A-51
15	33.4	6.2	858	13	US-10-027-632-323631

16	33.4	6.2	858	14	US-10-027-632-323631	Sequence 323631,
17	33.4	6.2	3681	13	US-10-085-418E-1	Sequence 1, Appli
18	33	6.2	661	13	US-10-027-632-229516	Sequence 229516,
19	33	6.2	661	13	US-10-027-632-229517	Sequence 229517,
20	33	6.2	661	14	US-10-027-632-229516	Sequence 229516,
21	33	6.2	661	14	US-10-027-632-229517	Sequence 229517,
22	32.6	6.1	6836	15	US-10-076-816-46	Sequence 46, Appl
23	32.6	6.1	659158	10	US-09-771-208-20	Sequence 20, Appl
24	32.2	6.0	23580	9	US-09-764-860-990	Sequence 990, App
25	32.2	6.0	23580	13	US-10-212-872-990	Sequence 990, App
26	32.2	6.0	23580	15	US-10-074-095-990	Sequence 990, App
27	32.2	6.0	38459	13	US-09-960-858-3	Sequence 3, Appli
28	32.2	6.0	38459	13	US-09-960-870-3	Sequence 3, Appli
29	32.2	6.0	580073	13	US-10-205-220-1	Sequence 1, Appli
30	31.6	5.9	562	9	US-09-864-761-15854	Sequence 15854, A
31	31.6	5.9	1125	10	US-09-967-768A-323	Sequence 323, App
32	31.6	5.9	1125	12	US-10-411-010-5	Sequence 5, Appli
33	31.6	5.9	1125	13	US-09-960-706-1057	Sequence 1057, Ap
34	31.6	5.9	1125	15	US-10-207-655-136	Sequence 136, App
35	31.6	5.9	1340	11	US-09-978-418-43	Sequence 43, Appl
36	31.6	5.9	2018	10	US-09-822-830A-597	Sequence 597, App
37	31.4	5.9	408	11	US-09-918-995-17612	Sequence 17612, A
38	31.4	5.9	2227	10	US-09-764-877-3516	Sequence 3516, Ap
39	31.4	5.9	2227	10	US-09-764-877-3519	Sequence 3519, Ap
40	31.4	5.9	2712	13	US-09-971-429B-46	Sequence 46, Appl
41	31.4	5.9	14171	10	US-09-764-877-3517	Sequence 3517, Ap
42	31.4	5.9	15998	10	US-09-764-877-3518	Sequence 3518, Ap
43	31	5.8	643	13	US-10-027-632-19603	Sequence 19603, A
44	31	5.8	643	14	US-10-027-632-19603	Sequence 19603, A
45	31	5.8	1621	13	US-10-027-632-258655	Sequence 258655,

ALIGNMENTS

RESULT 1  
US-10-124-591-2  
; Sequence 2, Application US/10124591  
; Publication No. US20020177208A1  
; GENERAL INFORMATION:  
; APPLICANT: Hawkins, Phillip R.  
; Bandman, Olga  
; Guegler, Karl J.  
; Shah, Purvi  
; Corley, Neil C.  
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/124,591  
; FILING DATE: 16-Apr-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/489,770  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/966,317  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0403 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 742 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: OVARUT01  
CLONE: 816403  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-124-591-2

Query Match 22.4%; Score 120; DB 14; Length 742;  
Best Local Similarity 68.0%; Pred. No. 3.2e-30;  
Matches 215; Conservative 0; Mismatches 90; Indels 11; Gaps 3;

QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGGTGTGACGAGGAGCTGGCTTACTGCTG 60  
DB 385 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGGTGTGACGAGGAGATTCCTAACTGCTTA 444  
QY 61 GCAGGACCGAGTACCACCTGAAATACCTCTTCTCCCTCCATTTTATGTGAGAAGGAC 120  
DB 445 GCCCAACTGAGTACAACCTTAAAGTACCTCTTCTACCCCGAGTTCCTATGTGAGCGGAC 504  
QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174  
DB 505 TCGCCCAAGTGTGACTGACTACCTTGACTTGAAATGCTCTTTGCACAGGAATAAAGC 564  
QY 175 TCACCTTCAGTGATCAACCAAGCATGCTTCTCCCTGCAAGTGTGACATGGAACGCACT 234  
DB 565 GTCTCTCAGTAATGAACAACAGCATTCAGTTATTTGCGAGA-AGGGAACCGAAGCAAGT 623  
QY 235 GCTAAAGCCA-----CCTGCGTTTGTGCTTCTCTCCCTGCAAGTGTGACGAGGAGTCAACACTATGAGC 290  
DB 624 GATAAAGCCACAACCTTGTGTGTTTGTCTTCCCTCCCAATCCCAAGTCAAGGAGCTGGAGCC 683  
QY 291 CTGTGAGTGTCCAGT 306  
DB 684 CATGTAGCTTGCAGT 699

RESULT 2  
US-09-962-832-63/c  
; Sequence 63, Application US/09962832  
; Patent No. US20020110821A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-74  
; CURRENT APPLICATION NUMBER: US/09/962,832  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,077  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,280  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 63  
; LENGTH: 445  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: n=a,t,g or c  
US-09-962-832-63

Query Match 17.6%; Score 94; DB 10; Length 445;  
Best Local Similarity 71.4%; Pred. No. 2.1e-21;  
Matches 140; Conservative 0; Mismatches 50; Indels 6; Gaps 1;

QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGGTGTGACGAGGAGCTGGCTTACTGCTG 60

DB 199 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGGTGTGACGAGGAGATTCCTAACTGCTTA 140  
QY 61 GCAGGACCGAGTACCACCTGAAATACCTCTTCTCCCTCCATTTTATGTGAGAAGGAC 120  
DB 139 GCCCAACTGAGTACAACCTTAAAGTACCTCTTCTACCCCGAGTTCCTATGTGAGCGGAC 80  
QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174  
DB 79 TCGCCCAAGTGTGACTGACTACCTTGACTTGAAATGCTCTTTTGCACAAGGAATAAAGC 20  
QY 175 TCACCTTCAGTGATCA 190  
DB 19 GTCCTCTCAGTAATGA 4

RESULT 3  
US-09-873-367C-205/c  
; Sequence 205, Application US/09873367C  
; Publication No. US20030165839A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; APPLICANT: Soppet, Daniel  
; APPLICANT: Endress, Gregory  
; APPLICANT: Augustus, Meena  
; APPLICANT: Ebner, Reinhard  
; APPLICANT: Carter, Kenneth  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
; TITLE OF INVENTION: Signature Gene Sets  
; FILE REFERENCE: 689290-64  
; CURRENT APPLICATION NUMBER: US/09/873,367C  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: U.S. 60/236,891  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: U.S. 60/236,842  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: U.S. 60/244,867  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: U.S. 60/245,084  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 1067  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 205  
; LENGTH: 445  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(445)  
; OTHER INFORMATION: n=a,t,g or c  
US-09-873-367C-205

Query Match 17.6%; Score 94; DB 13; Length 445;  
Best Local Similarity 71.4%; Pred. No. 2.1e-21;  
Matches 140; Conservative 0; Mismatches 50; Indels 6; Gaps 1;

QY 1 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGGTGTGACGAGGAGCTGGCTTACTGCTG 60  
DB 199 GCAGAGAACAAATGCCAAGAACTTTTGTGCAAGGTGTGACGAGGAGATTCCTAACTGCTTA 140  
QY 61 GCAGGACCGAGTACCACCTGAAATACCTCTTCTCCCTCCATTTTATGTGAGAAGGAC 120  
DB 139 GCCCAACTGAGTACAACCTTAAAGTACCTCTTCTACCCCGAGTTCCTATGTGAGCGGAC 80  
QY 121 TCTCCCAAGTCAATTGACAGGC-----TCACATGTCCCTTTGCACATGGAACGCACT 174  
DB 79 TCGCCCAAGTGTGACTGACTACCTTGACTTGAAATGCTCTTTTGCACAAGGAATAAAGC 20  
QY 175 TCACCTTCAGTGATCA 190  
DB 19 GTCCTCTCAGTAATGA 4

RESULT 4  
US-09-908-975-29871  
; Sequence 29871, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29871  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-29871

Query Match  
Best Local Similarity 11.9%; Score 63.4; DB 13; Length 65;  
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 412 TACCTGCTGCAGGGCTGCTGCAGATGGTGAACACTGCTTAGGCTTGGCTGGT 471  
Db 1 TACCTGCTGCAGGGCTGCTGCAGATGGTGAACACTGCTTAGGCTTGGCTGGT 471  
QY 472 AATAA 476  
Db 61 AATAA 65

RESULT 5  
US-10-027-632-155029/c  
; Sequence 155029, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 10827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 155029  
; LENGTH: 815  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-155029

US-10-027-632-155029

Query Match  
Best Local Similarity 7.0%; Score 37.4; DB 13; Length 815;  
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;  
QY 52 TACTGCCTGGCAGGACCGAGTACCACCTGAAATACCTCTTCTCCCTCCATTTATGT 111  
Db 667 TACAGACACCCAGGGTGCCATACCTCCAGGAGCACCTCTCTCCCTGCTTCTGTG 608  
QY 112 GAGAAGGACTCTCCCAAGTGAATGACAGGCTCACATGTCCCTTGCACATGGAACGC 171  
Db 607 GGCACAGCCACTCCAGGGCCGCGTGACACCTTTTGGAAAGCAGCCGCTTGCAGACAG 548  
QY 172 ACTTCACCTTTCAGTGATCACCACCAACAGCATGCAATTTGTGAGGAGAG 218  
Db 547 ATCATCCCTTTGAATCTCCCGCAGCAGCTGAACTTTGTCTTGAGGG 501

RESULT 6  
US-10-027-632-155029/c  
; Sequence 155029, Application US/10027632  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 10827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 155029  
; LENGTH: 815  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-155029

Query Match  
Best Local Similarity 7.0%; Score 37.4; DB 14; Length 815;  
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;  
QY 52 TACTGCCTGGCAGGACCGAGTACCACCTGAAATACCTCTTCTCCCTCCATTTATGT 111  
Db 667 TACAGACACCCAGGGTGCCATACCTCCAGGAGCACCTCTCTCCCTGCTTCTGTG 608  
QY 112 GAGAAGGACTCTCCCAAGTGAATGACAGGCTCACATGTCCCTTGCACATGGAACGC 171  
Db 607 GGCACAGCCACTCCAGGGCCGCGTGACACCTTTTGGAAAGCAGCCGCTTGCAGACAG 548  
QY 172 ACTTCACCTTTCAGTGATCACCACCAACAGCATGCAATTTGTGAGGAGAG 218  
Db 547 ATCATCCCTTTGAATCTCCCGCAGCAGCTGAACTTTGTCTTGAGGG 501

RESULT 7  
US-09-873-367C-444/c  
; Sequence 444, Application US/09873367C  
; Publication No. US20030165839A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; APPLICANT: Soppet, Daniel



Mon Dec 22 13:23:38 2003

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Query Match      6.6%; Score 35.2; DB 15; Length 1830121;
Best Local Similarity 49.5%; Pred. No. 43;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 201 GCAATTTGTCAGGAGAGTCAACGGAGGCAAGTGCTAAAGCCACCTGCGTTTGCTTTCT 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1392777 GAAGTTTATCCATGCAAGAACGCGTTGCGTTTCATCTAATGATTTCTTGAATATATTTT 1392718

Qy 261 CCTTCCATTACGAACTCACAACATATAGCCTGTGGAGTTGCCAGTCTGATGAAGTTTCA 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1392717 CGCTTCATCATGATGAATAAGGGATGTTTGATCTTTTGGCGCTGAGAGTAAACCGCA 1392658

Qy 321 AAGTCTGGCGCTGTTTATACAAATAAGCGCTGTGTGGCGTGGTATACTTTTGTGAAA 380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1392657 AAGTTCTTGTACCGTAAATGCGGATTATCTCCAAAGTAGGCGCGGCTTACTTCTGGGAT 1392598

Qy 381 TTCA 384
    ||||
Db 1392597 TTCA 1392594
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RESULT 10
US-10-027-632-290510
; Sequence 290510, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290510
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-290510
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Query Match      6.5%; Score 34.6; DB 13; Length 630;
Best Local Similarity 58.1%; Pred. No. 0.68;
Matches 61; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 292 TGTGGAGTTGCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTTTATACAAATAAGCG 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 TGTGGTCTGTGCTCAGATGTAACCTTCTGTATCTGGGCAATTTCTAATAAACATTTT 504

Qy 352 CTGTGTTGGCGTGGTATACTTTTGAATTCAGCCTTTATGAGA 396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 CTCTGTGATTTTGGTAGGAATCTAAATTCAGCCTTTCTCAAA 549
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RESULT 11
US-10-027-632-290510
; Sequence 290510, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290510
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-290510
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```
Query Match      6.5%; Score 34.6; DB 14; Length 630;
Best Local Similarity 58.1%; Pred. No. 0.68;
Matches 61; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 292 TGTGGAGTTGCCAGTCTGATGAAGTTCAAAGTCTGGGCTGTTTATACAAATAAGCG 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 445 TGTGGTCTGTGCTCAGATGTAACCTTCTGTATCTGGGCAATTTCTAATAAACATTTT 504

Qy 352 CTGTGTTGGCGTGGTATACTTTTGAATTCAGCCTTTATGAGA 396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 505 CTCTGTGATTTTGGTAGGAATCTAAATTCAGCCTTTCTCAAA 549
```

```
RESULT 12
US-10-027-632-290511
; Sequence 290511, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290511
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-290511
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Db. 479 GACAGAGACTCATCTTTAAATGTCTTGGGTAGAACCAAAAAAAAAA 525

Search completed: December 19, 2003, 14:10:51  
Job time : 271 secs